

(54) A colorectal cancer suppressor gene related protein

(57) [Abstract]

[PROBLEM TO BE SOLVED] To discover a novel substance that is associated with the colorectal tumor suppressor gene APC in order to enable control of APC and to control colorectal tumors.

[SOLUTION] A novel protein M1 having an ability to bind to the APC gene product, particularly to the armadillo repeat (Arm) domain of the gene product, which is namely a polypeptide consisting of the amino acid sequence set forth in SEQ ID No: 1 of the Sequence Listing, a polypeptide containing part of the polypeptide, a polynucleotide encoding the polypeptide or its complementary strand, a vector containing the polynucleotide or its complementary strand, a transformant containing the vector, an antibody against the polypeptide, a method for producing the polypeptide, a method for screening inhibitors, an antagonist and activator of the function and expression of M1 using the aforementioned products, and a compound identified by the method are provided, and further a pharmaceutical composition and diagnostic means for use in colorectal tumors are provided using the aforementioned products.

[0009] Furthermore, the novel protein M1 was found to have, as a function thereof, GEF activity specific to Rac, a member of the Rho family. Namely, the novel protein M1 binds to Rac to promote GDP/GTP exchange reaction and activates Rac, and further acts on NF  $\kappa$ B, c-jun, SRE, etc. located downstream of cell signaling in which Rac is involved. Besides, the novel protein M1 may induce cell lamellipodia and membrane ruffling that result from the physiological function of Rac, and thus its involvement in cell adhesion is presumed.

[0010] Regarding the localization of the APC gene product within a cell, it is reported that the APC gene product accumulates at the ends of microtubules in the migrating cell when the cell migrates from the crypt to the tip of intestinal villus (J. Cell Biol., 134:165-179, 1996). The novel protein M1 of the present invention has been found to accumulate also in similar areas within the cell. These facts raise the possibility that the novel protein M1 of the present invention holds a key to the regulation of cell migration in intestinal villus.

[0027] (Screening) The novel protein M1 thus prepared and the polypeptide derived therefrom, the polynucleotide encoding thereof and its complementary strand, the cell transformed based on the information about the amino acid sequences and base sequences thereof, and the antibody that immunologically recognizes the novel protein M1 or the polypeptide derived therefrom provide, when using them solely or in combination, an effective means to screen for an inhibitor or activator that acts on the binding of the novel protein M1 and the polypeptide derived therefrom to the APC gene product, the function of

the novel protein M1 including its GEF activity, or the expression of the novel protein M1. Namely, it is possible to provide a screening method to obtain a compound that inhibits or enhances the binding of the polypeptide of the present invention to the APC gene product utilizing at least either of the polypeptide or the antibody of the present invention; a screening method for a compound that reacts with the polynucleotide of the present invention and inhibits or enhances the expression of the polynucleotide utilizing at least any one of the polynucleotide, the vector, the transformant, and the antibody of the present invention; and a screening method for a compound that inhibits or enhances the function of the polypeptide of the present invention including the GEF activity utilizing at least either of the polypeptide and the antibody of the present invention. For example, the screening of an antagonist by the drug design based on the stereo-structure of the polypeptide, the screening of an expression-regulating agent by gene level using a protein-synthesizing system, and the screening of an antibody-recognizing substance using an antibody, can be carried out by using one of well-known drug-screening systems.

[0029] The candidate compounds thus selected can be used in preparing a pharmaceutical composition for use in the treatment of colorectal tumors by selecting ones by taking a balance between their biological usefulness and toxicity into consideration. Besides, the novel protein M1 and the polypeptide derived therefrom, the polynucleotide encoding thereof and its complementary strand, the vector containing the nucleotide sequence thereof, and the antibody that immunologically recognizes the novel protein M1 and the polypeptide derived therefrom can be used themselves as a pharmaceutical means for use in treating colorectal tumors which have a function to inhibit, to antagonize, or to activate the interaction of the novel protein M1 with the APC gene product. Here, colorectal tumors include both benign and malignant tumors, specifically exemplified by familial adenomatous polyposis (FAP) and colon cancer. For the pharmaceutical preparation, it is sufficient to use a well-known means suitable for preparing each of the objects such as peptide, protein, polynucleotide, or antibody.

[0044] (Localization of M1 within a cell) Next, the novel protein M1 of the present invention was studied for its localization within a cell. First, a Madin-Darby canine kidney (MDCK) epithelial cell line was cultured in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum (FBS). cDNAs of full-length M1 and M1 $\Delta$ NB (amino acids 127-619) were subcloned into pcDNA 3.1(+) that is a mammalian expression vector having a CMV promotor. Plasmid DNA, pMKITneo-Myc-tagged APC-arm, was constructed by inserting a DNA fragment encoding a partial sequence of APC (amino acids 446-880) into pMKITneo having a SR $\alpha$  promotor. The expression plasmid was transfected into MDCK cells by using LipofectAMINE (Life Technologies Co.) according to the instruction manual.

[0045] MDCK cells were fixed with 3.7% formaldehyde in phosphate buffered saline (PBS) at 4°C for one hour. The fixed cells were treated with Tris-buffered saline (TBS) containing 0.2% triton X-100 at room temperature for 10 minutes and washed three times with TBS.

After permeabilization, the cells were incubated with a primary antibody in TBS containing 1% BSA, 3% FBS and 0.2% triton X-100 at room temperature for one hour. After removing the primary antibody, the cells were washed three times with TBS. Bound primary antibody was detected by using a goat secondary antibody (Cappel Co.) labeled with FITC (fluorescein isothiocyanate) or rhodamine. The stained samples were examined under a Carl Zeiss LSM510 Laser scanning microscope.

[0046] The results are shown in Fig. 9. The cell shown in Fig. 9a is the same as that shown in Fig. 9b, which was made to express HA-tagged M1 protein. The cell shown in Fig. 9c is the same as that shown in Fig. 9d, which was made to express both HA-tagged M1 protein and Myc-tagged APC-arm. The cell shown in Fig. 9e is a cell that was made to express HA-tagged M1 $\Delta$ NB (amino acids 127-619). The cell shown in Fig. 9f is a cell that was made to express Myc-tagged APC-arm. The cell shown in Fig. 9a and Fig. 9b was double-stained with an anti-HA antibody and an anti-APC antibody. The cell shown in Fig. 9c and Fig. 9d was double stained with an anti-HA antibody and an anti-Myc antibody. The cell shown in Fig. 9e was treated with an anti-HA antibody. The cell shown in Fig. 9f was treated with an anti-Myc antibody. As indicated by arrowheads in Fig. 9b, clusters of APC protein were present in membrane extensions. Furthermore, as indicated by arrows in Fig. 9a ~ d, M1 and APC proved to be co-localized at the same area of the epithelial cell periphery.

[0047] (Morphological analysis of M1 expressing cell line) Furthermore, an MDCK cell line stably expressing M1 $\Delta$ NB was established to examine the effect of M1 on cell morphology and cytoskeleton. Five clones of the M1 $\Delta$ NB expressing cell line all showed a tendency to grow dispersedly without closely aggregating to each other. The novel protein M1 was presumed to be involved in cell adhesion.

[0048]

[EFFECT OF THE INVENTION] As explained above, M1 of the present invention is a novel protein that characteristically binds to the armadillo repeat domain of the APC gene product and possesses GEF (guanine nucleotide exchange factor) activity. A novel pharmaceutical composition and a diagnostic means that use such characteristics above will provide great usefulness in the clinical and basic medical field relating to the APC gene product.

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(54)【発明の名称】 大腸癌抑制遺伝子関連蛋白質

(57)【要約】

【課題】大腸癌抑制遺伝子A P Cに関する新規物質を見いだし、A P Cの制御を可能にし、大腸癌を制御すること。

【解決手段】A P C遺伝子産物、特に該遺伝子産物のアルマジロリピート(A r m)部位との結合能をもつ新規蛋白質M 1、すなわち配列表の配列番号1に示すアミノ酸配列からなるポリペプチド、及び該ポリペプチドの一部を有するポリペプチド、該ポリペプチドをコードするポリヌクレオチドまたはその相補鎖、該ポリヌクレオチドまたはその相補鎖を含むベクター、該ベクターを有する形質転換体、当該ポリペプチドに対する抗体、当該ポリペプチドの製造法、上記のものを利用したM 1の機能および発現の阻害剤・拮抗剤・賦活剤のスクリーニング方法、該方法で同定された化合物を提供し、更にこれらを利用し、大腸腫瘍に用いる医薬組成物・診断手段を提供する。

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## 【特許請求の範囲】

【請求項 1】 下記の群より選ばれるポリペプチド：

①配列表の配列番号 1 に記載のアミノ酸配列で示されるポリペプチド、

②前記①のポリペプチドのアミノ酸配列を含有するポリペプチド、

③前記①のポリペプチドと少なくとも約 70% のアミノ酸配列上の相同性を有しあつ大腸癌の癌抑制遺伝子 (Adenomatous Polyposis Coli : APC) の遺伝子産物のアルマジロリピート部位をコードするポリペプチドに対する結合能を有するポリペプチド、および

④前記①から③のポリペプチドのアミノ酸配列において 1 ないし数個のアミノ酸の消失、置換、付加などの変異あるいは誘発変異を有し、かつ APC 遺伝子産物のアルマジロリピート部位に対する結合能を有するポリペプチド。

【請求項 2】 配列表の配列番号 1 に記載のアミノ酸配列の少なくとも 5 個のアミノ酸配列を有し、かつ APC 遺伝子産物のアルマジロリピート部位に対する結合能を有するポリペプチド。

【請求項 3】 請求項 1 または 2 に記載のポリペプチドをコードするポリヌクレオチドまたはその相補鎖。

【請求項 4】 請求項 3 に記載のポリヌクレオチドまたはその相補鎖とストリンジメントな条件下でハイブリダイゼーションするポリヌクレオチド。

【請求項 5】 配列表の配列番号 2 に記載のポリヌクレオチドまたはその相補鎖の塩基配列のうち少なくとも 1 5 個の連続した塩基配列で示されるポリヌクレオチドであって、該ポリヌクレオチドの転写によって発現されるポリペプチドが APC 遺伝子産物のアルマジロリピート部位に対する結合能を有する、ポリヌクレオチド。

【請求項 6】 請求項 3 から 5 のいずれか 1 項に記載のポリヌクレオチドを含有する組換えベクター。

【請求項 7】 請求項 6 の組換えベクターで形質転換された形質転換体。

【請求項 8】 請求項 7 の形質転換体を培養する工程を含む、請求項 1 または 2 に記載のポリペプチドの製造方法。

【請求項 9】 請求項 1 または 2 に記載のポリペプチドを免疫学的に認識する抗体。

【請求項 10】 請求項 1 に記載のポリペプチドの、 APC 遺伝子産物のアルマジロリピート部位に対する結合能を阻害もしくは増強する化合物のスクリーニング方法であって、請求項 1 または 2 に記載のポリペプチド、請求項 9 に記載の抗体のうち、少なくともいずれか 1 つを用いることを特徴とするスクリーニング方法。

【請求項 11】 請求項 3 もしくは 4 に記載のポリヌクレオチドと相互作用して該ポリヌクレオチドの発現を阻害もしくは増強する化合物のスクリーニング方法であつ

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て、請求項 3 から 5 のいずれか 1 項に記載のポリヌクレオチド、請求項 6 に記載のベクター、請求項 7 に記載の形質転換体、請求項 9 に記載の抗体のうち少なくともいずれか 1 つを用いることを特徴とするスクリーニング方法。

【請求項 12】 請求項 1 に記載のポリペプチドの GEF (グアニンヌクレオチド交換因子: Guanine nucleotide Exchange Factor) 活性を阻害もしくは増強する化合物のスクリーニング方法であって、請求項 1 または 2 に記載のポリペプチド、請求項 9 に記載の抗体のうち少なくともいずれか 1 つを用いることを特徴とするスクリーニング方法。

【請求項 13】 請求項 10 から 12 のいずれか 1 項に記載のスクリーニング方法でスクリーニングされる化合物。

【請求項 14】 請求項 1 に記載のポリペプチドの、 APC 遺伝子産物のアルマジロリピート部位に対する結合性を阻害もしくは増強する化合物。

【請求項 15】 請求項 3 から 5 のいずれか 1 項に記載のポリヌクレオチドと相互作用して該ポリヌクレオチドの発現を阻害もしくは増強する化合物。

【請求項 16】 請求項 1 に記載のポリペプチドの GEF 活性を阻害もしくは増強する化合物。

【請求項 17】 請求項 1 または 2 に記載のポリペプチド、請求項 3 から 5 のいずれか 1 項に記載のポリヌクレオチド、請求項 6 に記載のベクター、請求項 7 に記載の形質転換体、請求項 9 に記載の抗体、または請求項 13 から 16 のいずれか 1 項に記載の化合物のうち、少なくともいずれか 1 つを含有することを特徴とする、大腸腫瘍の治療に用いる医薬組成物。

【請求項 18】 請求項 1 のポリペプチドの発現または活性に関連した疾病的診断手段であって、試料中の

(a) 該ポリペプチドをコードしているポリヌクレオチド、および／または (b) 該ポリペプチド、をマーカーとして分析することを含む診断手段。

## 【発明の詳細な説明】

## 【0001】

【産業上の利用分野】 本発明は、大腸癌に関する癌抑制遺伝子 (Adenomatous Polyposis Coli : APC) がコードするポリペプチドに対する結合能、特に APC 遺伝子産物のアルマジロリピート部位に対する結合能を有する新規な蛋白質（以下、M1 と呼称する）およびポリペプチドに関するものである。さらに詳しくは、新規蛋白質 M1 のアミノ酸配列の全部または一部を有するポリペプチド、該ポリペプチドをコードするポリヌクレオチド、該ポリヌクレオチドを含有する組換えベクター、該組換えベクターで形質転換された形質転換体、該形質転換体を使ったペプチドまたはポリペプチドの製造方法、該ペプチドまたはポリペプチドに対する抗体、これらを利用した化合物のスクリー

ニング方法、該スクリーニングされた化合物、該ポリペプチド若しくは該ポリヌクレオチドに作用する活性阻害化合物または活性賦活化合物、これらに関係する医薬組成物、およびこれらに関係する疾病診断手段に関する。

## 【0002】

【従来の技術】癌抑制遺伝子APCは、家族性腺腫性ポリポーシス (familial adenomatous polyposis: FAP) の原因遺伝子として単離され、散発性の大腸癌の70~80%では、該APCの異常が報告されている。APC遺伝子産物は、2,843個のアミノ酸からなる300kDaの巨大な蛋白質である (Cell, 87: 159-170, 1996) (Nature, 382: 638-642, 1996)。APC遺伝子産物は、種々の蛋白質との相互作用が知られており、その1つにβ-カテニンがある。β-カテニンは、カドヘリンの細胞質側ドメインに結合して細胞接着に役割を果たすと同時に、発生過程や腫瘍形成において重要な役割を担うWnt/Winglessシグナル伝達経路の重要な構成要素の1つとしても機能している (Cell, 86: 391-399, 1996) (Science, 275: 1784-1787, 1997) (Science, 275: 1787-1790, 1997) (Science, 275: 1790-1792, 1997)。その他、APC遺伝子産物は、GSK-3b、Axinもしくはコンダクチン/Axinとの相互作用が知られている (Science, 280: 596-599, 1998) (Current Biology, 8: 573-581, 1998) (J. Biol. Chem., 273: 10823-10826, 1998) (Genes Cells, 6: 395-403, 1998)。また、APC遺伝子産物は、EB1とhDLGとの、そのC末端を介した相互作用も報告されている (Science, 272: 1020-1023, 1996)。さらに、APC遺伝子産物には、蛋白質間の相互作用の役割を担うアルマジロリピートドメインが存在することも知られている。

## 【0003】

【発明が解決しようとする課題】本発明が解決しようとする課題は、上記のように多様な物質との相互作用を担う大腸癌の癌抑制遺伝子であるAPC遺伝子に関する新規物質を見いだすことであり、該新規物質を癌の制御を目的とする手段として使用することである。より具体的には、本発明の課題はAPC遺伝子産物との結合能、特にAPC遺伝子産物由來のアルマジロリピートドメインとの結合能、をもつ新規な物質(M1)を提供することであり、それに伴い有用性ある新規物質(M1)由来

のポリペプチドを提供することである。また本発明の別の課題は、M1由来のポリペプチドをコードするポリヌクレオチドを提供し、遺伝子工学手法による、M1由来のポリペプチドの製造法を提供することである。さらに本発明の別の課題は、M1由来のポリペプチドに対する抗体を提供することである。その他の本発明の課題は、上記のものを利用してM1の有する作用の阻害剤・拮抗剤・賦活剤のスクリーニングをおこなうことであり、スクリーニングされた化合物を提供することであり、またこれらを利用した大腸腫瘍に用いる医薬組成物・診断手段を提供することである。

## 【0004】

【解決するための手段】課題解決のため、本発明者は、ヒト胎児脳cDNAライブラリーからAPC遺伝子産物のアルマジロリピートドメイン（以下、armと呼称することもある）に結合する新規蛋白質M1のcDNAを2ハイブリッドスクリーニング法を用いて同定し、その塩基配列および該新規蛋白質M1のcDNAがコードするアミノ酸配列を決定し、本発明を完成した。

【0005】すなわち、本発明は下記の群より選ばれるポリペプチド：①配列表の配列番号1に記載のアミノ酸配列で示されるポリペプチド、②前記①のポリペプチドのアミノ酸配列を含有するポリペプチド、③前記①のポリペプチドと少なくとも約70%のアミノ酸配列上の相同性を有しあつ大腸癌の癌抑制遺伝子 (Adenomatous Polyposis Coli: APC) の遺伝子産物のアルマジロリピート部位をコードするポリペプチドに対する結合能を有するポリペプチド、および④前記①から③のポリペプチドのアミノ酸配列において1ないし数個のアミノ酸の欠失、置換、付加などの変異あるいは誘発変異を有し、かつAPC遺伝子産物のアルマジロリピート部位に対する結合能を有するポリペプチド；配列表の配列番号1に記載のアミノ酸配列の少なくとも5個のアミノ酸配列を有し、かつAPC遺伝子産物のアルマジロリピート部位に対する結合能を有するポリペプチド；本発明のポリペプチドをコードするポリヌクレオチドまたはその相補鎖；本発明のポリヌクレオチドまたはその相補鎖とストリングエントな条件下でハイブリダイゼーションするポリヌクレオチド；本発明のポリヌクレオチドまたはその相補鎖の塩基配列のうち少なくとも15個の連続した塩基配列で示されるポリヌクレオチドであって、該ポリヌクレオチドの転写によって発現されるポリペプチドがAPC遺伝子産物のアルマジロリピート部位に対する結合能を有する、ポリヌクレオチド；本発明のポリヌクレオチドを含有する組換えベクター；本発明の組換えベクターで形質転換された形質転換体；本発明の形質転換体を培養する工程を含む、本発明のポリペプチドの製造方法；本発明のポリペプチドのAPC遺伝子産物のアルマジロリピート部位に対する結合性を阻害もしくは増強する化合物のスクリーニング方法

であって、本発明のポリペプチド、本発明の抗体のうち少なくともいずれか1つを用いることを特徴とするスクリーニング方法；本発明のポリヌクレオチドと相互作用して該ポリヌクレオチドの発現を阻害もしくは増強する化合物のスクリーニング方法であって、本発明のポリヌクレオチド、本発明のベクター、本発明の形質転換体、本発明の抗体のうち少なくともいずれか1つを用いることを特徴とするスクリーニング方法；本発明のポリペプチドのG E F (グアニンヌクレオチド交換因子：G u a n i n e n u c l e o t i d e E x c h a n g e F a c t o r) 活性を阻害もしくは増強する化合物のスクリーニング方法であって、本発明のポリペプチド、本発明の抗体のうち少なくともいずれか1つを用いることを特徴とするスクリーニング方法；本発明のスクリーニング方法でスクリーニングされる化合物；本発明のポリペプチドのA P C遺伝子産物のアルマジロリピート部位に対する結合性を阻害もしくは増強する化合物；本発明のポリヌクレオチドと相互作用して該ポリヌクレオチドの発現を阻害もしくは増強する化合物；本発明のポリペプチドのG E F活性を阻害もしくは増強する化合物；本発明のポリペプチド、本発明のポリヌクレオチド、本発明のベクター、本発明の形質転換体、本発明の抗体、または本発明の化合物のうち少なくともいずれか1つを含有することを特徴とする大腸腫瘍の治療に用いる医薬組成物；本発明のポリペプチドの発現または活性に関連した疾病的診断手段であって、試料中の(a)該ポリペプチドをコードしているポリヌクレオチド、および/または(b)該ポリペプチド、をマーカーとして分析することを含む診断手段、を提供する。

## 【0006】

【発明の実施の形態】(新規M1) 本発明において提供される新規蛋白質M1をコードするポリヌクレオチドは、ヒトの胎児脳cDNAライブラリーから、A P C遺伝子産物のアルマジロリピートドメインを使い、2ハイブリッドスクリーニング法により、新規なアミノ酸配列を有する物質として、そのcDNAが取得されたものである。本発明の新規蛋白質M1のcDNAは、619個のアミノ酸からなる蛋白質をコードし、既知のD b I ファミリー(低分子量G蛋白質Rhoファミリーに作用するGDP解離促進蛋白質の1つである) (Current Opinion in Cell Biology, 8: 216-222, 1996) に類似のドメイン構造を有していた。遺伝子データベース(The National Center for Biotechnology Information)を検索したところ、本発明の新規蛋白質M1のcDNAは、D b I ファミリーの1つである既知物質KIAA0424と約73%の相同性を有することが判明した。KIAA0424は、本発明の新規蛋白質M1とは、該M1のN末端領域を欠如する点に最も大きな差異を有する。両者は、D b 50

I相同(D H)ドメイン、ブレックストリン(P r e c k s t r i n)相同(P H)ドメイン、S r c相同3(S H 3)ドメインを担持する点において同一である。また、マウスを用いた新規蛋白質M1の組織分布研究において、該M1のm R N Aが脳に高レベルで発現しており、他の臓器でも低レベルで発現していることを確認した。

【0007】新規蛋白質M1のペプチド断片(配列表、配列番号1のアミノ酸73~126)を使用して作製した抗体は、グルタチオン-S-トランスフェラーゼ(G S T)との融合蛋白として得た新規蛋白質M1に対し強い反応性を示した。また、該作製した抗体を用い、脳に存在する新規物質M1が、約85kDaの蛋白質であることを抗原抗体反応を利用して測定系で確認した。

【0008】また、新規蛋白質M1とA P C遺伝子産物との直接的な相互作用を確認するための実験において、グルタチオン-S-トランスフェラーゼ(G S T)との融合蛋白として得たA P C遺伝子産物のアルマジロリピートドメイン(A P C-a r m)は、G S T融合M1断片(G S T-M1-M)と相互作用したが、G S T単独とは反応せず、同様に、M1-Mは、G S T-A P C-a r mとは反応したが、G S T融合β-カテニンのアルマジロリピートドメイン又はG S T単独とは反応しないことを確認した。すなわち、新規蛋白質M1はA P C遺伝子産物と、該A P C遺伝子産物のアルマジロリピートドメインを介して結合していると推定される。また、ラット胎児脳の溶解物(I y s a t e)を抗A P C抗体で免疫沈降し、ついで抗M1抗体でイムノプロットすることにより、A P C遺伝子産物と本発明のM1が共沈殿する

ことが判明した。この反応において、抗M1抗体を、抗原性を保持するM1断片で前処理すると、M1とA P C遺伝子産物の共沈殿が阻害された。すなわち、M1とA P C遺伝子産物とは生体内で結合していると考えられる。また、M1とA P C遺伝子産物の結合部位を2ハイブリッド法を用いて確認したところ、少なくともM1のアミノ酸73~126で示される領域に結合部位が存在することが推定された。このことは、M1のS H 3ドメインの上流域に、A P C遺伝子産物のアルマジロリピートドメインとの結合部位が存在することを意味する。KIAA0424は、このような領域をもたないので、A P C遺伝子産物との反応性がない。

【0009】さらに、新規蛋白質M1はその作用として、Rhoファミリーの1つであるR a cに特異的なG E F活性をもつことを確認した。つまり、新規蛋白質M1は、R a cに結合しG D P/G T P交換反応を促進してR a cを活性化し、R a cの関与する細胞情報伝達の下流に位置するN F κB、c-j u n、S R E等に作用する。また、R a cの生理機能である、細胞のラメリポディア(葉状仮足)や細胞膜のラッピングを誘導する可能性もあり、細胞接着への関与が推定される。

【0010】APC遺伝子産物の細胞内局在については、細胞が大腸絨突起先端へクリプトから移動する際に、移動する細胞の微小管先端部位に集積していることが報告されている（J. Cell Biol., 134: 165-179, 1996）が、本発明の新規蛋白質M1も同様の部位に集積していることを見出した。このことから、本発明の新規蛋白質M1が、大腸絨突起における細胞移動制御の鍵を握っている可能性がある。

【0011】（ポリペプチド）本発明の新規蛋白質M1は、配列表の配列番号1に示すアミノ酸配列からなるポリペプチドである。さらに本発明のポリペプチドは、この配列表の配列番号1に示すポリペプチドの部分配列を有するポリペプチドから選択される。その選択されるポリペプチドは、配列表の配列番号1に示すポリペプチドと、好ましくは約70%以上、より好ましくは約80%以上、さらに好ましくは約90%をこえる相同性を有する。この相同性をもつポリペプチドの選択は、例えばAPC遺伝子産物のアルマジロリピートドメインとの結合性を指標にして行うことができる。

【0012】アミノ酸配列の相同性を決定する技術は、自体公知であり、例えばアミノ酸配列を直接決定する方法、推定されるポリヌクレオチドの塩基配列を決定後これにコードされるアミノ酸配列を推定する方法等を使用することができる。

【0013】本発明のポリペプチドは、配列表の配列番号1に示すアミノ酸配列からなるポリペプチドの、部分配列を有するポリペプチドから選択されるアミノ酸配列を試薬・標準物質・免疫原として利用できる。その最小単位としては、少なくとも約5個以上、好ましくは少なくとも約8~10個以上、さらに好ましくは少なくとも約11~15個以上のアミノ酸で構成されるアミノ酸配列からなり、免疫学的にスクリーニングしうるポリペプチドを本発明の対象とする。

【0014】さらに、このように特定されたポリペプチドをもとにして、APC遺伝子産物のアルマジロリピートドメインとの結合性を指標とすることにより、1ないし数個のアミノ酸の欠失・置換・付加などの変異あるいは誘発変異を有するアミノ酸配列からなるポリペプチドも提供することができる。欠失・置換・付加あるいは挿入の手段は自体公知であり、例えばUImmerの技術（Science, 219: 666, 1983）を利用してることが出来る。さらに、これら利用できるペプチドは、その構成アミノ基もしくはカルボキシル基などを修飾するなど、機能の著しい変更を伴わない程度に改変が可能である。

【0015】本発明のポリペプチドは、それら自体で、新規蛋白質M1の機能を調節するための医薬組成物に使用できる。また、本発明のポリペプチドは、新規蛋白質M1の機能を調節しうる化合物、例えば、阻害剤、拮抗剤、賦活剤等を得るためにスクリーニングや、新規蛋白質M1に対する抗体の取得に用いることができる。さらに、本発明のポリペプチドは、試薬・標準品としても使用可能である。

質M1に対する抗体の取得に用いることができる。さらに、本発明のポリヌクレオチドは、試薬・標準品としても使用可能である。

【0016】（ポリヌクレオチド）本発明のポリヌクレオチドおよびその相補鎖は、配列表の配列番号1に記載のアミノ酸配列をコードする、配列表の配列番号2のポリヌクレオチドおよび該ポリヌクレオチドに対する相補鎖、これらのポリヌクレオチドとストリンジェントな条件下でハイブリダイゼーションするポリヌクレオチド、およびこれらのポリヌクレオチドのうち少なくとも15個の連続した塩基配列を有しかつコードするペプチドがAPC遺伝子産物のarmドメインとの結合能を有するポリヌクレオチド、を意味する。ポリヌクレオチドとしてDNAを代表例にとると、「DNAにストリンジェントな条件下でハイブリダイズするDNA」は、例えば前述のMolecular Cloningに記載の方法によって得ることができる。ここで、「ストリンジェントな条件下でハイブリタイズする」とは、例えば、6×SSC、0.5%SDSおよび50%ホルムアミドの溶液中で42°Cにて加温した後、0.1×SSC、0.5%SDSの溶液中で68°Cにて洗浄する条件でも依然として陽性のハイブリタイズのシグナルが観察されることを表す。

【0017】本発明のポリヌクレオチドは、配列表の配列番号1に記載のアミノ酸配列をコードする、配列表の配列番号2のポリヌクレオチドの情報から選択される相補鎖および相補鎖を意味し、指定されたヌクレオチド配列の領域に対応する少なくとも約15~20個以上の配列からなるポリヌクレオチド配列及び該相補鎖を意味する。この有用なポリヌクレオチド配列の決定は、公知の蛋白質発現系、例えば無細胞蛋白質発現系を利用して簡単に発現蛋白質の確認を行い、その生理活性特にAPC遺伝子産物のアルマジロリピートドメインとの結合性を指標にして選別することにより行うことができる。無細胞蛋白質発現系としては、例えば胚芽、家兎網状赤血球等由来のリボソーム系の技術を利用できる（Nature, 179, 160~161, 1957）。

【0018】これらのポリヌクレオチドは、いずれも本発明の新規蛋白質M1および本発明のポリペプチドの製造に有用な遺伝子情報を提供するものであり、これらをコードする遺伝子等の核酸、またはmRNA検出のためのプローブもしくはプライマーとして、あるいは遺伝子発現を調節するためのアンチセンスオリゴマーとして使用することができる。例えば、本発明のポリヌクレオチドをアンチセンスとして使用する場合、他の既知蛋白質、例えばDbIファミリーの1つであるKIAA0424等、とのコンセンサス配列領域以外の新規蛋白質M1に固有な領域のヌクレオチド配列を用いることにより、M1の発現が特異的に阻害される。さらに、本発明のポリヌクレオチドは、核酸に関する試薬・標準品とし

ても利用できる。

【0019】(形質転換体) 上記のような無細胞蛋白質発現系以外にも、大腸菌、酵母、枯草菌、昆虫細胞、動物細胞等の自体公知の宿主を利用した遺伝子組換え技術によって、本発明からなる新規蛋白質M1およびその由来物からなるポリペプチドを提供可能である。本発明の具体例においては、COS-7細胞を利用したが、無論これに限定されるものではない。

【0020】形質転換は、自体公知の手段を応用することができ、例えばレブリコンとして、プラスミド、染色体、ウイルス等を利用して宿主の形質転換を行う。より好ましい系としては、遺伝子の安定性を考慮するならば、染色体内へのインテグレート法があげられるが、簡便には核外遺伝子を用いた自律複製系を利用する。ベクターは、宿主の種類により選択され、発現目的の遺伝子配列と複製そして制御に関する情報を担持した遺伝子配列とを構成要素とする。構成要素は宿主が原核細胞か真核細胞かによって選択し、プロモーター、リボソーム結合部位、ターミネーター、シグナル配列、エンハンサー等を自体公知の方法によって組合せて使用する。

【0021】形質転換体は、自体公知の各々の宿主の培養条件に最適な条件を選択して培養することにより、本発明のポリペプチドの製造に用いることができる。培養は、発現產生される新規蛋白質M1およびその由来物からなるポリペプチドの生理活性、特にAPC遺伝子産物のアルマジロリピートドメインとの結合性を指標にして行ってもよいが、培地中の形質転換体量を指標にして継代培養またはバッチによって行う。

【0022】(新規蛋白質M1およびその由来物の回収) 培地からの新規蛋白質M1およびその由来物からなるポリペプチドの回収は、APC遺伝子産物のアルマジロリピートドメインとの結合性を指標にして、分子篩、イオンカラムクロマトグラフィー、アフィニティクロマトグラフィー等を組合せるか、溶解度差にもとづく疏安、アルコール等の分画手段によっても精製回収できる。より好ましくは、アミノ酸配列の情報に基づき、該アミノ酸配列に対する抗体を作成し、ポリクローナル抗体またはモノクローナル抗体によって、特異的に吸着回収する方法を用いる。

【0023】(抗体) 抗体は、本発明の新規蛋白質M1およびその由来物からなるポリペプチドの抗原決定基を選別し、作成する。抗原決定基は、少なくとも5個、より好ましくは少なくとも8~10個のアミノ酸で構成される。このアミノ酸配列は、必ずしも配列表の配列番号1と相同である必要はなく、蛋白質の立体構造上の外部への露出部位であればよく、露出部位が不連続部位であれば、該露出部位について連続的なアミノ酸配列であることも有効である。実施例では、アミノ酸配列の73位~126位の断片を免疫原として利用した。抗体は、免疫学的に新規蛋白質M1およびその由来物からなるポリ

ペプチドを認識する限り特に限定されない。この認識の有無は、公知の抗原抗体結合反応によって決定する。

【0024】抗体を产生するためには、本発明の新規蛋白質M1およびその由来物からなるポリペプチドを、アジュバントの存在または非存在下で、単独または担体に結合して、動物に対して体液性応答および/または細胞性応答等の免疫誘導を行う。担体は、自身が宿主に対して有害作用をおこさなければ特に限定されず、例えばセルロース、重合アミノ酸、アルブミン等が例示される。免疫する動物としては、マウス、ラット、兎、やぎ、馬等が好適に用いられる。ポリクローナル抗体は、自体公知の血清からの抗体回収法によって取得する。好ましい手段としては、免疫アフィニティーコロマトグラフィー法である。実施例においては、GST-M1を結合させたアフィニティーコロマトグラフィーにより、抗M1抗体を精製した。

【0025】モノクローナル抗体を生産するためには、上記の免疫手段が施された動物から抗体産生細胞を回収し、自体公知の永久増殖性細胞への形質転換手段を導入することによって行われる。

【0026】ポリクローナル抗体またはモノクローナル抗体は、直接本発明からなる新規蛋白質M1と結合し、その活性を制御可能であり、APC遺伝子産物と新規蛋白質M1との相互作用系の制御を容易に行うことができる。そのため、APC遺伝子産物と新規蛋白質M1が関連する疾患の治療・予防のために有用である。

【0027】(スクリーニング) かくして調製された新規蛋白質M1およびその由来物からなるポリペプチド、これらをコードするポリヌクレオチドおよびその相補鎖、これらのアミノ酸配列および塩基配列の情報に基づき形質転換させた細胞、並びに新規蛋白質M1およびその由来物からなるポリペプチドを免疫学的に認識する抗体は、単独または複数手段を組合せることによって、新規蛋白質M1およびその由来物からなるポリペプチドとAPC遺伝子産物との結合性、新規蛋白質M1のGEF活性等の機能、または新規蛋白質M1の発現に対する阻害剤もしくは賦活剤のスクリーニングに有効な手段を提供する。すなわち、本発明のポリペプチド、本発明の抗体の少なくともいずれか1つを用いることで、本発明のポリペプチドとAPC遺伝子産物との結合性を阻害もしくは増強する化合物を得るためのスクリーニング方法が、本発明のポリヌクレオチド、本発明のベクター、本発明の形質転換体、本発明の抗体の少なくともいずれか1つを用いることで本発明のポリヌクレオチドと相互作用し該ポリヌクレオチドの発現を阻害もしくは増強する化合物のスクリーニング方法が、本発明のポリペプチド、本発明の抗体の少なくともいずれか1つを用いることで本発明のポリペプチドのGEF活性等の機能を阻害もしくは増強する化合物のスクリーニング方法が提供可能である。例えば、ポリペプチドの立体構造に基づくド

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ラグデザインによる拮抗剤の選別、蛋白質発現系を利用した遺伝子レベルでの発現調整剤の選別、抗体を利用した抗体認識物質の選別等が、自体公知の医薬品スクリーニングシステムにおいて利用可能である。

【0028】(化合物、医薬組成物) 上記のスクリーニング方法で得られた化合物は、新規蛋白質M1およびその由来物からなるポリペプチドとAPC遺伝子産物との相互作用、または新規蛋白質M1のG E F活性等の機能を調節する阻害剤、拮抗剤、賦活剤等の候補化合物として利用可能である。また、遺伝子レベルでの新規蛋白質M1およびその由来物からなるポリペプチドの発現に対する阻害剤、拮抗剤、賦活剤等の候補化合物としても利用可能である。上記の阻害剤、拮抗剤、賦活剤等の候補化合物としては、蛋白質、ポリペプチド、抗原性を有さないポリペプチド、低分子化合物等が挙げられ、好ましくは低分子化合物である。

【0029】かくして選別された候補化合物は、生物学的有用性と毒性のバランスを考慮して選別することによって、大腸腫瘍の治療に用いる医薬組成物として調製可能である。また、本発明からなる新規蛋白質M1およびその由来物からなるポリペプチド、これらをコードするポリヌクレオチドおよびその相補鎖、これらの塩基配列を含むベクター並びに、新規蛋白質M1およびその由来物からなるポリペプチドを免疫学的に認識する抗体は、それら自体が、新規蛋白質M1とAPC遺伝子産物との相互作用に対する阻害・拮抗・賦活等の機能を有する、大腸腫瘍の治療に用いる医薬手段として使用できる。ここで、大腸腫瘍とは、良性腫瘍ならびに悪性腫瘍を含み、具体的には、家族性腺腫性ポリポーシス(FAP)および大腸癌が挙げられる。なお、製剤化にあたっては、自体公知のポリペプチド、蛋白質、ポリヌクレオチド、抗体等、各対象に応じた製剤化手段を導入すればよい。

【0030】本発明からなる新規蛋白質M1およびその由来物からなるポリペプチド、これらをコードするポリヌクレオチドおよびその相補鎖、これらの塩基配列を含むベクター並びに、新規蛋白質M1およびその由来物からなるポリペプチドを免疫学的に認識する抗体は、本発明のポリペプチドの発現またはその活性が関連する疾患、例えば、本発明の新規蛋白質M1の発現またはAPC遺伝子産物との相互作用に関連した疾患等の診断手段として使用することができる。特に、大腸腫瘍の診断マーカーおよび/または試薬等の診断手段として有用である。診断は、新規蛋白質M1をコードしている核酸配列との相互作用・反応性を利用して、相応する核酸配列の存在量を決定すること、および/または新規蛋白質M1について生体内分布を決定すること、および/または新規蛋白質M1の試料中での存在量を決定することによって行う。詳しくは、新規蛋白質M1を診断マーカーとして検定する。その測定法は、自体公知の抗原抗体反応

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系、酵素反応系、PCR反応系等を利用すればよい。なお、ここで言う手段とは、目的達成のために使用する方法および/または媒体を意味する。すなわち、例えば、診断手段には、診断するための方法、診断に用いる試薬キットなどが含まれる。

【0031】

【実施例】以下、本発明を実施例に基づき具体的に説明するが、本発明は下記の実施例に限定されない。

(cDNAのクローニング) APC遺伝子産物のアルマジロリピートドメイン(以下、APC-armと略称することもある)に対する結合能を有する蛋白質を得ることを目的として、2ハイブリッドスクリーニング(two hybrid screens)(CLONTECH MATCHMAKER™ Two-Hybrid System)を行った。すなわち、ベイト(bait)として、ヒトAPC遺伝子産物アルマジロリピートドメイン(アミノ酸残基446-880)を融合させたGAL4 DNA結合ドメインを含有するプラスミドGBT9-APCを用い、ヒト胎児脳(human fetal brain)cDNAライブラリー(Clontech)を対象としてスクリーニングした。該cDNAライブラリーとベイトとを、レポーター遺伝子としてhis3とlacZとを導入した酵母にトランスフェクションし、β-galアッセイおよびHIS栄養要求性を指標として、陽性クローリーを検出した。

【0032】形質転換体1、 $1 \times 10^7$  個から、1つの陽性クローリーを得た。この得られたクローリーから、該クローリーで発現されているAPC-armに結合するポリペプチドをコードするcDNA断片の塩基配列をDNAシークエンスにより決定したところ、新規な配列であった。得られたcDNA断片の下流領域の配列は'Marathon-ready'ヒト脳cDNA(Clontech)を用いて3'RACEシステム(Clontech)により取得した。プライマーは5'-CGACATCTGCGAGGGCTACGTCCGG-3'を用いた。また上記で得られたcDNA断片の配列の一部(配列表、配列番号2の塩基番号97-269)をプローブとして、ヒトゲノムライブラリー(Clontech)について、ジゴキシゲニン(digoxigenin; DIG)標識プローブを用いたハイブリダイゼーションによりスクリーニングした。その結果、配列表、配列番号2の塩基番号1-81を含む2つのオーバーラップするクローリーを得、目的とするAPC-armに結合する蛋白質の完全長cDNAの配列を決定した。

【0033】(アミノ酸配列) 上記方法で得られた、配列表の配列番号2に示すcDNAは新規な塩基配列を有していた。該cDNAをもとに、その塩基配列の翻訳によって、新規蛋白質M1の推定アミノ酸配列、すなわち配列表の配列番号1に示すアミノ酸残基619の配列が得られた(図1A)。

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【0034】(既存蛋白質との相同性) 該新規蛋白質M1の推定アミノ酸配列を用いて、既存の database (Genbank) に対してBLAST (The National Center for Biotechnology Information) を用いた相同性検索を行ったところDb1ファミリーのサブファミリーメンバーの1つであるKIAA0424と73%の相同性を認めた(図2B, C)。両者は、Db1相同(Db1 homology: DH) ドメイン、プレックストリン相同(Preckstrin homolog: PH) ドメイン、Src相同3(SH3) ドメインを保持する点において同一であるが、KIAA0424には、新規蛋白質M1のN末端領域は存在しないことが判明した。この結果、配列表の配列番号1に示すアミノ酸配列を有する本発明の蛋白質M1は新規蛋白質であることが確認された。

【0035】(発現組織の確認) 次に配列表の配列番号1の推定アミノ酸配列で示される新規蛋白質M1の、ヒト組織における発現を、ノザンプロット解析により確認した。多種のヒト組織から得たpoly(A)+RNAをプロットしたフィルターをClontech社より入手し、DIG標識したM1のcDNAプローブ、5'-GACCACACTGCCATCGCTG-3'および5'-TGTAGTTACCAAGGACCG-3'でハイブリダイゼーションした。その結果、脳に高レベルで発現していることを確認した。また、tissue blotによる解析では、脳以外に、睾丸でも存在を確認した。さらに、腎由来の細胞でも発現を確認した。

【0036】(抗体の产生) M1に対する抗体は、NZWウサギをM1のアミノ酸73-126を含むペプチドを用いて公知の方法で免疫し調製した。APCに対する抗体は、NZWウサギをAPC遺伝子産物(以下APCと略称することもある)のアミノ酸1122-1729を含むペプチドを用いて公知の方法で免疫して調製した。APCのN末端領域に対するマウスモノクローナル抗体は公知の方法で調製した(Miyashiro et al., 1995)。抗体は、それぞれ免疫に用いた抗原を結合させたアフィニティカラムを使用してアフィニティクロマトグラフィーを行うことにより精製した。精製したウサギポリクローナル抗M1抗体とGST融合M1(GST-M1)との結合反応性を調べたところ、得られた抗体は、GST-M1に強い反応性を示した。

【0037】(M1の発現) 本発明の新規蛋白質M1を発現させるために、発現プラスミドpCDNA3.1 (+) のEcoRI/NotI部位にM1のcDNAを組み込み、COS-7細胞にトランスクレクションし

5'-ATTTATTGTAGTTACCAAGGAC-3'  
5'-TGCCTGAAGCACTCTGGGAC-3'

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た。新規蛋白質M1の発現確認のため、M1 cDNAを組み込んだベクター、コントロールベクター、HA-タグで標識したM1 cDNAを組み込んだベクター、HA-タグを組み込んだベクターを、COS-7細胞にトランスクレクションした。培養した各形質転換体の溶解物、およびM1の存在が確認されているラット胎児脳の溶解物について、上記の様に取得した抗M1抗体、および抗HA抗体を用いて免疫沈降し、SDS-PAGEにより分画し、次いで抗M1抗体および抗HA抗体を用いてイムノプロットを行った。M1 cDNAを組み込んだベクター(レーン3)、HA-タグで標識したM1 cDNAを組み込んだベクター(レーン6、8)で形質転換したCOS-7細胞およびラット胎児脳(レーン1)では明らかに新規蛋白質の発現が認められ、その分子量は約85 kDaであることが判明した(図2)。また、用いた抗M1抗体を抗原で事前処理しておく(図2中、p.e.p. 士で表示)と、新規蛋白質は検出されなかった。すなわち、抗M1抗体で認識される新規蛋白質M1が発現されたことが確認された。

【0038】(M1とAPCとのin vivoにおける結合の解析) ラット胎児脳溶解物について、上記で作製した新規蛋白質M1、およびAPCに対するウサギポリクローナル抗体、ならびに $\beta$ -カテニンに対するマウスモノクローナル抗体(Transduction Laboratories)を用いて免疫沈降し、SDS-PAGEにより各沈降物を分離後、各抗体を用いてイムノプロットを行った(図3)。レーン1および2はラット胎児脳の溶解物を抗M1抗体で、レーン3および4は抗APC抗体で、レーン5および6は抗 $\beta$ -カテニン抗体で免疫沈降した結果を、レーン1、3、5は、予め各抗体を対応する抗原で吸収して用いた結果(図3中、p.e.p. 士で表示)を示す。抗M1抗体で免疫沈降したM1が抗APC抗体もしくは抗 $\beta$ -カテニン抗体で検出され、抗APC抗体で免疫沈降したAPC遺伝子産物が抗M1抗体で検出され、抗 $\beta$ -カテニン抗体で免疫沈降した $\beta$ -カテニンが抗M1抗体で検出されることから、新規蛋白質M1はin vivoにおいてもAPCおよび $\beta$ -カテニンと結合していることが明らかとなった。

【0039】(M1とAPCの相互作用部位の解析) 新規蛋白質M1の、APC結合ドメインの解析を行うため、M1の様々な欠失変異体(deletion mutant)を公知の方法で作製し、APCとの結合領域を酵母(yeast)を用いた2ハイブリッドシステムにより調べた。具体的には、M1の欠失変異体を、下記の特異的なプライマーを用いPCRを行って、pGAD424にクローニングし、GAL4活性化ドメインとの融合体を作成した。

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5' -GACCA CACTGCCATCGCTGATG-3'  
 5' -CCTCAGCCGAACGAAAGCTGGCTG-3'  
 5' -CTTGCTGCTCTGC G C T C C G C -3'  
 5' -GTGAATCAGGACGAGCCC GCG-3'  
 5' -GATGTTCCCGAAGATGGTACG-3'  
 5' -ATGCCTGATGGAGCTCTGGAC-3'

ついで、該GAL4活性化ドメインとの融合体を2ハイブリッドシステムにおいてHIS3 auxotrop hyと $\beta$ -galリポーター活性を用いて、その相互作用を試験した。その結果、図4に示すように、SH3の上流の領域にAPC結合部位が存在することが判明した。

【0040】(M1とRhoファミリー低分子量G蛋白質との結合解析)新規蛋白質M1は、Db1ファミリーのサブファミリーの1つであるKIAA0424と高い相同意を有する。Db1ファミリーは低分子量G蛋白質の1つであるRhoファミリーに作用するGDP解離促進蛋白質である。新規蛋白質M1と、KIAA0424との相同意に着目し、新規蛋白質M1の機能解析のため、Rhoファミリー低分子量G蛋白質(small G protein; RhoA, Rac1, CDC42)との結合を調べた。ニッケルビーズに吸着させた新規蛋白質M1をRhoA, Rac1およびGST-CD C42と、0.1%NP-40を含むE1A緩衝液[50mM HEPES, pH7, 0, 150mM NaCl, 50mM NaF, 5mM EDTA, 1mMDTT, 50μg/mL phenylmethylsulfonyl fluoride (PMSF), 1μg/ml ロイペプチド, 1μg/mlアプロチニン]中で4°Cにて1時間混合し、共沈殿物をイムノプロッティングで検出した。図5に示すように、陽性コントロールとして使用したDb1は用いた全てのRhoファミリー低分子量G蛋白質と結合するが、新規蛋白質M1はRhoAおよびRac1とは結合したが、CDC42とは結合しなかった。

【0041】(M1のGEF活性)次に、新規蛋白質M1のGEF活性について検討した。低分子量G蛋白質からのGDP解離を調べるために使用する [<sup>3</sup>H] GDP結合型の低分子量G蛋白質を、2pmolの各低分子量G蛋白質を0.2μM [<sup>3</sup>H] GDPと30°Cで20分間、導入用緩衝液>Loading buffer; 20mM Tris-HCl, pH8, 0, 3mM MgCl<sub>2</sub>, 10mM EDTAおよび1mMジチオスレイトール) 中でインキュベートすることにより得た。低分子量G蛋白質からの [<sup>3</sup>H] GDPの解離を防ぐために、375mM MgCl<sub>2</sub>を終濃度が18mMとなるように加え、直ちに、該混合液を氷冷した。 [<sup>3</sup>H] GDPの解離は、反応溶液(20mM Tris-HCl, pH8, 0, 6mM MgCl<sub>2</sub>, 3.5mM EDTAおよび1mM ジチオスレイトール)に250倍過剰の

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非標識GDP、GTPおよびM1を加えることにより25°Cで行った(図6A, B)。次に、低分子量G蛋白質へのGTPの結合を調べるために使用するGDP結合型の低分子量G蛋白質を、2pmolの各低分子量G蛋白質を0.2μM非標識GDPと30°Cで20分間、導入用緩衝液>Loading buffer) 中でインキュベートし、375mM MgCl<sub>2</sub>を終濃度が18mMとなるように加えることにより得た。 [<sup>35</sup>S] GTPSの、GDP結合型低分子量G蛋白質への結合は、10μMの [<sup>35</sup>S] GTPSおよびM1を反応溶液に加えることにより、25°Cで実施した(図7A, B)。解離試験、結合試験の両方において、反応は1mIの氷冷した停止用緩衝液(20mM Tris-HCl, pH8, 0, 25mM MgCl<sub>2</sub>および100mM NaCl)を加えて、停止した。希釈した混合溶液をニトロセルロースろ紙で濾過し、フィルターを数回、停止用緩衝液で洗浄した。ろ纸上に捕捉された放射活性をカウントした。タンパク質濃度はウシ血清アルブミン(BSA)を標準蛋白質として用いて測定した。

【0042】図6に示すように、新規蛋白質M1は、結合しうる低分子量G蛋白質であるRac1に作用して、Rac1からのGDP解離を促進したが(図6A)、RhoAには結合しないのでRhoAからのGDP解離には作用しなかった(図6B)。また、図7に示すように、新規蛋白質M1は、Rac1へのGTP結合を促進した(図7A)が、RhoAへのGTP結合には影響しなかった(図7B)。すなわち、本発明の新規蛋白質M1は、低分子量G蛋白質に作用し、GEF活性を有する。

【0043】(M1のGEF活性に対するAPCの作用)さらに、様々な濃度のM1について、APC-armの存在下または非存在下で、20nMの [<sup>3</sup>H] GDPを結合させた結合型のRac1からの [<sup>3</sup>H] GDP解離促進能を30°Cで15分間インキュベーションして測定した。APC-armはM1より過剰量、モル比で5倍となるように加えた。図8に示すように、M1のGDP解離促進能は、APC-armの添加により、増強された。すなわち、M1は、APCと結合することにより、GDP解離促進能が増強されることが示唆された。

【0044】(M1の細胞内局在)次に、本発明の新規蛋白質M1の細胞内局在について検討した。まず、Madin-Darby canine kidney (MDCK) 上皮細胞株を10%ウシ胎児血清(FBS)を含むDulbecco's modified Eagle

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Le's medium (DMEM) 中で培養した。全長のM1およびM1△NB (アミノ酸127-619) cDNAはCMVプロモーターを有する哺乳動物発現ベクターpcDNA3.1 (+) 中にサブクローニングした。プラスミドDNA、pMKITNEo-Mycタグで標識したAPC-armは、APC (アミノ酸446-880) の部分配列をコードしているDNA断片をSRαプロモーターを有するpMKITNEoに挿入することにより構築した。発現プラスミドは、リポフェクトアミン (Lipofect AMINE; Life Technologies社) を用いて、使用者マニュアルにしたがって、MDCK細胞にトランスフェクトした。

【0045】MDCK細胞は、リン酸緩衝生理食塩水 (Phosphate Buffered Saline; PBS) 中で3.7%ホルムアルデヒドを用いて4°Cで1時間、固定した。固定した細胞は室温で10分間、0.2%トリトンX-100を含むトリス緩衝生理食塩水 (Tris Buffered Saline; TBS) で処理し、TBSで3回洗浄した。細胞を透過化した (permeabilize) 後、1%BSA、3%FBS、0.2%トリトンX-100を含むTBS中で一次抗体と室温で1時間、インキュベートした。一次抗体を除去し、細胞をTBSで3回洗浄した。結合した一次抗体は、FITC (Fluorescein isothiocyanate) またはローダミンを結合したヤギ二次抗体 (Cappel社) を用いて、検出した。染色したサンプルは、カールツァイス LSM510レーザー走査顕微鏡 (Carl Zeiss LSM510 Laser scanning microscope) 下で、観察した。

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30 【配列表】

## Sequence Listing

<110> Daiichi Pharmaceutical Co.,Ltd.  
<120> Colon carcinoma suppressor gene related protein  
<130> DP99-1045  
<160> 2  
<210> 1  
<211> 619  
<212> PRT  
<213> human  
<400> 1  
Met Arg Pro Asp Gly Gln Gln Ala Leu Asp Ala Val Val Arg Ser Phe  
1 5 10 15  
Asp Cys His Ser Glu Ala Ala Leu Arg Gln Arg Asn Asp Val Ile Tyr  
20 25 30  
Cys Ser Leu Pro Arg Thr Ala Gln Gly Ile Val Gln Arg Glu Asp Gln  
35 40 45  
Leu Glu Val Leu Val Ser Leu Arg Glu Val Trp Gly Arg Arg Arg Gly  
50 55 60  
Arg Asp Gly Thr Cys Thr Gly Ala Met Pro Asp Gly Ala Leu Asp Thr  
65 70 75 80

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【0046】結果は、図9に示す。図9中、a、bはHAタグで標識したM1蛋白質を発現させた同一細胞、c、dはHAタグで標識したM1蛋白質とMyo-cタグで標識したAPC-armとを両方発現させた同一細胞、eはHAタグで標識したM1△NB (アミノ酸127-619) を発現させた細胞、fはMyo-cタグで標識したAPC-armを発現させた細胞である。また、a、bは抗HA抗体と抗APC抗体で二重染色し、c、dは抗HA抗体と抗Myo-c抗体で二重染色し、eは抗HA抗体で、fは抗Myo-c抗体で処理した。b中の矢印頭で示すように、APC蛋白質のクラスターが伸長している膜中に存在しており、また、a～d中の矢印で示すように、M1とAPCが上皮細胞中で細胞の辺縁の同一部位に共存していることが判明した。

【0047】(M1発現細胞株の形態解析) さらに、M1△NBを安定に発現するMDCK細胞株を樹立し、M1が細胞の形態、骨格に与える影響を調べたところ、M1△NB発現細胞株5クローニングはいずれも密に接着せばらばらに増殖する傾向が見られた。新規蛋白質M1の細胞接着への関与が推定された。

【0048】

【発明の効果】以上説明したように本発明のM1は、新規蛋白質であり、そのAPC遺伝子産物のアルマジロリピート部位との結合性が特徴的で、GEF (グアニンヌクレオチド交換因子: Guanine nucleotide Exchange Factor) 活性を有する。この特性を利用した新規医薬組成物、診療手段の提供は、APC遺伝子産物関連の臨床・基礎の医用領域において大きな有用性を提供する。

Ala Val Cys Ala Asp Glu Val Gly Ser Glu Glu Asp Leu Tyr Asp Asp  
                  85                     90                     95  
 Leu His Ser Ser His His Tyr Ser His Pro Gly Gly Gly Glu  
                  100                 105                 110  
 Gln Leu Ala Ile Asn Glu Leu Ile Ser Asp Gly Ser Val Val Cys Ala  
                  115                 120                 125  
 Glu Ala Leu Trp Asp His Val Thr Met Asp Asp Gln Glu Leu Gly Phe  
                  130                 135                 140  
 Lys Ala Gly Asp Val Ile Glu Val Met Asp Ala Thr Asn Arg Glu Trp  
                  145                 150                 155                 160  
 Trp Trp Gly Arg Val Ala Asp Gly Glu Gly Trp Phe Pro Ala Ser Phe  
                  165                 170                 175  
 Val Arg Leu Arg Val Asn Gln Asp Glu Pro Ala Asp Asp Asp Ala Pro  
                  180                 185                 190  
 Leu Ala Gly Asn Ser Gly Ala Glu Asp Gly Gly Ala Glu Ala Gln Ser  
                  195                 200                 205  
 Ser Lys Asp Gln Met Arg Thr Asn Val Ile Asn Glu Ile Leu Ser Thr  
                  210                 215                 220  
  
 Glu Arg Asp Tyr Ile Lys His Leu Arg Asp Ile Cys Glu Gly Tyr Val  
                  225                 230                 235                 240  
 Arg Gln Cys Arg Lys Arg Ala Asp Met Phe Ser Glu Glu Gln Leu Arg  
                  245                 250                 255  
 Thr Ile Phe Gly Asn Ile Glu Asp Ile Tyr Arg Cys Gln Lys Ala Phe  
                  260                 265                 270  
 Val Lys Ala Leu Glu Gln Arg Phe Asn Arg Glu Arg Pro His Leu Ser  
                  275                 280                 285  
 Glu Leu Gly Ala Cys Phe Leu Glu His Gln Ala Asp Phe Gln Ile Tyr  
                  290                 295                 300  
 Ser Glu Tyr Cys Asn Asn His Pro Asn Ala Cys Val Glu Leu Ser Arg  
                  305                 310                 315                 320  
 Leu Thr Lys Leu Ser Lys Tyr Val Tyr Phe Phe Glu Ala Cys Arg Leu  
                  325                 330                 335  
 Leu Gln Lys Met Ile Asp Ile Ser Leu Asp Gly Phe Leu Leu Thr Pro  
                  340                 345                 350  
 Val Gln Lys Ile Cys Lys Tyr Pro Leu Gln Leu Ala Glu Leu Leu Lys  
                  355                 360                 365  
 Tyr Thr His Pro Gln His Arg Asp Phe Lys Asp Val Glu Ala Ala Leu  
                  370                 375                 380  
  
 His Ala Met Lys Asn Val Ala Gln Leu Ile Asn Glu Arg Lys Arg Arg  
                  385                 390                 395                 400  
 Leu Glu Asn Ile Asp Lys Ile Ala Gln Trp Gln Ser Ser Ile Glu Asp  
                  405                 410                 415  
 Trp Glu Gly Glu Asp Leu Leu Val Arg Ser Ser Glu Leu Ile Tyr Ser  
                  420                 425                 430  
 Gly Glu Leu Thr Arg Val Thr Gln Pro Gln Ala Lys Ser Gln Gln Arg  
                  435                 440                 445  
 Met Phe Phe Leu Phe Asp His Gln Leu Ile Tyr Cys Lys Lys Asp Leu  
                  450                 455                 460

Leu Arg Arg Asp Val Leu Tyr Tyr Lys Gly Arg Leu Asp Met Asp Gly  
 465 470 475 480  
 Leu Glu Val Val Asp Leu Glu Asp Gly Lys Asp Arg Asp Leu His Val  
 485 490 495  
 Ser Ile Lys Asn Ala Phe Arg Leu His Arg Gly Ala Thr Gly Asp Ser  
 500 505 510  
 His Leu Leu Cys Thr Arg Lys Pro Glu Gln Lys Gln Arg Trp Leu Lys  
 515 520 525  
 Ala Phe Ala Arg Glu Arg Glu Gln Val Gln Leu Asp Gln Glu Thr Gly  
 530 535 540  
 Phe Ser Ile Thr Glu Leu Gln Arg Lys Gln Ala Met Leu Asn Ala Ser  
 545 550 555 560  
 Lys Gln Gln Val Thr Gly Lys Pro Lys Ala Val Gly Arg Pro Cys Tyr  
 565 570 575  
 Leu Thr Arg Gln Lys His Pro Ala Leu Pro Ser Asn Arg Pro Gln Gln  
 580 585 590  
 Gln Val Leu Val Leu Ala Glu Pro Arg Arg Lys Pro Ser Thr Phe Trp  
 595 600 605  
 His Ser Ile Ser Arg Leu Ala Pro Phe Arg Lys \*  
 610 615 620  
 <210> 2  
 <211> 1860  
 <212> cDNA  
 <213> human  
 <400> 2  
 atg agg cca gat ggg cag caa gct ttg gat gct gtg gta agg agt ttt 48  
 Met Arg Pro Asp Gly Gln Gln Ala Leu Asp Ala Val Val Arg Ser Phe  
 1 5 10 15  
 gac tgt cac tct gaa gca gct ctc agg cag agg aat gat gtg att tat 96  
 Asp Cys His Ser Glu Ala Ala Leu Arg Gln Arg Asn Asp Val Ile Tyr  
 20 25 30  
 tgt agt tta cca agg acc gct cag ggt att gtg cag agg gaa gac cag 144  
 Cys Ser Leu Pro Arg Thr Ala Gln Gly Ile Val Gln Arg Glu Asp Gln  
 35 40 45  
 ctg gag gtt ctt gtg tca ctc cgt gaa gtg tgg ggg cgg cgg agg ggc 192  
 Leu Glu Val Leu Val Ser Leu Arg Glu Val Trp Gly Arg Arg Arg Gly  
 50 55 60  
 aga gat ggg acc tgc act gga gcc atg cct gat gga gct ctg gac aca 240  
 Arg Asp Gly Thr Cys Thr Gly Ala Met Pro Asp Gly Ala Leu Asp Thr  
 65 70 75 80  
 gct gtc tgc gct gac gaa gtg ggg agc gag gag gac ctg tat gat gac 288  
 Ala Val Cys Ala Asp Glu Val Gly Ser Glu Glu Asp Leu Tyr Asp Asp  
 85 90 95  
 ctg cac agc tcc agc cac cac tac agc cac cct gga ggg egt ggg gag 336  
 Leu His Ser Ser Ser His His Tyr Ser His Pro Gly Gly Gly Glu  
 100 105 110  
 cag ctg gct atc aat gag ctc atc agc gat ggc agt gtg gtc tgc gct 384  
 Gln Leu Ala Ile Asn Glu Leu Ile Ser Asp Gly Ser Val Val Cys Ala  
 115 120 125  
 gaa gca ctc tgg gac cat gtc acc atg gac gac cag gag ctg ggc ttc 432

Glu Ala Leu Trp Asp His Val Thr Met Asp Asp Gln Glu Leu Gly Phe			
130	135	140	
aaa gct ggg gac gtc atc gaa gtg atg gat gcc acc aac aga gag tgg		480	
Lys Ala Gly Asp Val Ile Glu Val Met Asp Ala Thr Asn Arg Glu Trp			
145	150	155	160
tgg tgg ggc cgg gtc gcc gat ggc gag ggc tgg ttt cca gcc agc ttc		528	
Trp Trp Gly Arg Val Ala Asp Gly Glu Gly Trp Phe Pro Ala Ser Phe			
165	170	175	
gtt cgg ctg agg gtg aat cag gac gag ccc gcg gat gac gac gcc cct		576	
Val Arg Leu Arg Val Asn Gln Asp Glu Pro Ala Asp Asp Asp Ala Pro			
180	185	190	
ctg gcc ggg aac agc gga gcg gag gac ggc ggg gog gag gcg cag agc		624	
Leu Ala Gly Asn Ser Gly Ala Glu Asp Gly Gly Ala Glu Ala Gln Ser			
195	200	205	
agc aag gac cag atg cgg acc aac gtc atc aac gag atc ctc agc act		672	
Ser Lys Asp Gln Met Arg Thr Asn Val Ile Asn Glu Ile Leu Ser Thr			
210	215	220	
gag cgg gac tac atc aag cac ctg cgc gac atc tgc gag ggc tac gtc		720	
Glu Arg Asp Tyr Ile Lys His Leu Arg Asp Ile Cys Glu Gly Tyr Val			
225	230	235	240
cgg cag tgc cgc aag cgc gca gac atg ttc agc gag gag cag ctg cgt		768	
Arg Gln Cys Arg Lys Arg Ala Asp Met Phe Ser Glu Glu Gln Leu Arg			
245	250	255	
acc atc ttc ggg aac atc gag gac atc tac cgc tgc cag aag gcc ttc		816	
Thr Ile Phe Gly Asn Ile Glu Asp Ile Tyr Arg Cys Gln Lys Ala Phe			
260	265	270	
gtg aag gcc ctg gag cag agg ttc aac cgc gag cgc cca cac ctg agc		864	
Val Lys Ala Leu Glu Gln Arg Phe Asn Arg Glu Arg Pro His Leu Ser			
275	280	285	
gag ctg ggt gcc tgc ttc ctg gag cat caa gcc gac ttc cag atc tac		912	
Glu Leu Gly Ala Cys Phe Leu Glu His Gln Ala Asp Phe Gln Ile Tyr			
290	295	300	
tcg gag tac tgc aat aac cac ccc aac gcc tgc gtg gag ctc tcc cgg		960	
Ser Glu Tyr Cys Asn Asn His Pro Asn Ala Cys Val Glu Leu Ser Arg			
305	310	315	320
ctc acc aag ctc agc aag tac gtg tac ttc ttc gag gcc tgc cgg ctg		1008	
Leu Thr Lys Leu Ser Lys Tyr Val Tyr Phe Phe Glu Ala Cys Arg Leu			
325	330	335	
ctg cag aag atg att gac atc tcc ctg gat ggc ttc ctg ctg act cog		1056	
Leu Gln Lys Met Ile Asp Ile Ser Leu Asp Gly Phe Leu Leu Thr Pro			
340	345	350	
gtg cag aag atc tgc aag tac cct ctg cag ctg gcc gag ctg ctc aaa		1104	
Val Gln Lys Ile Cys Lys Tyr Pro Leu Gln Leu Ala Glu Leu Leu Lys			
355	360	365	
tac acg cac ccc cag cac agg gac ttc aag gat gtt gaa gcc gcc ttg		1152	
Tyr Thr His Pro Gln His Arg Asp Phe Lys Asp Val Glu Ala Ala Leu			
370	375	380	
cat gcc atg aag aac gtc gcc cag ctc atc aac gag cgg aag cgg aga		1200	

His Ala Met Lys Asn Val Ala Gln Leu Ile Asn Glu Arg Lys Arg Arg			
385	390	395	400
ctt gag aac atc gac aag att gct cag tgg cag agc tcc ata gag gac			1248
Leu Glu Asn Ile Asp Lys Ile Ala Gln Trp Gln Ser Ser Ile Glu Asp			
405	410	415	
tgg gag gga gaa gat ctc ttg gtc agg agc tca gaa ctc atc tac tcg			1296
Trp Glu Gly Glu Asp Leu Leu Val Arg Ser Ser Glu Leu Ile Tyr Ser			
420	425	430	
ggg gag ctg act cga gtt aca cag cct caa gcc aaa agc cag cag cga			1344
Gly Glu Leu Thr Arg Val Thr Gln Pro Gln Ala Lys Ser Gln Gln Arg			
435	440	445	
atg ttc ttt ctc ttt gac cac cag ctc atc tac tgt aag aag gac ctg			1392
Met Phe Phe Leu Phe Asp His Gln Leu Ile Tyr Cys Lys Lys Asp Leu			
450	455	460	
ctc cgc cgc gac gtg ttg tac tac aag ggc cgg ctg gac atg gac ggc			1440
Leu Arg Arg Asp Val Leu Tyr Tyr Lys Gly Arg Leu Asp Met Asp Gly			
465	470	475	480
ctg gag gtg gtg gac ctg gag gac ggg aag gac aga gac ctc cat gtg			1488
Leu Glu Val Val Asp Leu Glu Asp Gly Lys Asp Arg Asp Leu His Val			
485	490	495	
agc atc aag aac gcc ttc cgg ctg cac cgt ggc gcc aca ggg gac agc			1536
Ser Ile Lys Asn Ala Phe Arg Leu His Arg Gly Ala Thr Gly Asp Ser			
500	505	510	
cac ctg ctg tgc acc agg aag ccc gag cag aag cag cgc tgg ctc aag			1584
His Leu Leu Cys Thr Arg Lys Pro Glu Gln Lys Gln Arg Trp Leu Lys			
515	520	525	
gcc ttt gcc agg gag agg gag cag gtg cag ctg gac cag gag aca ggc			1632
Ala Phe Ala Arg Glu Arg Glu Gln Val Gln Leu Asp Gln Glu Thr Gly			
530	535	540	
ttc tcc atc act gaa ctg cag agg aag cag gac atg ctg aat gcc agc			1680
Phe Ser Ile Thr Glu Leu Gln Arg Lys Gln Ala Met Leu Asn Ala Ser			
545	550	555	560
aag cag cag gtc aca ggg aag ccc aaa gct gtt ggc cgg ccc tgc tac			1728
Lys Gln Gln Val Thr Gly Lys Pro Lys Ala Val Gly Arg Pro Cys Tyr			
565	570	575	
ctg acg cgc cag aag cac cca gcc ctg ccc agc aac cgg ccc cag cag			1776
Leu Thr Arg Gln Lys His Pro Ala Leu Pro Ser Asn Arg Pro Gln Gln			
580	585	590	
cag gtc ctg gtg ctg gcg gag ccc agg cgc aag cca tct acc ttc tgg			1824
Gln Val Leu Val Leu Ala Glu Pro Arg Arg Lys Pro Ser Thr Phe Trp			
595	600	605	
 cac agc atc agc cgg ctg gca ccc ttc cgc aag tga			1860
His Ser Ile Ser Arg Leu Ala Pro Phe Arg Lys *			
610	615	620	

## 【図面の簡単な説明】

【図1】 新規蛋白質M1のアミノ酸配列の特徴および  
相同ドメインの配列比較を説明する図である。(A) ヒ  
トM1の推定アミノ酸配列。SH3ドメインは太字、D  
Hドメインは囲み太字、PHドメインは太字かつ下線で

表示する。(B) M1と、DbIファミリーのサブファ  
ミリーメンバー; KIAA0424、DbI、Tiam  
-1、Vav、p115-RhoGEF、CDC24お  
よびSos1との比較。DHドメインの相同性はM1の  
50 DHドメインとほかのタンパクのDHドメインとの対応

比較における同一性／相同性の割合として計算した。

(C) DHドメインのアミノ酸配列表。M1、KIAA0424、DbI、Tiam-1、Vav、p115-RhoGEF、CDC24およびSos1のDHドメインを並列し、さらに最適化した。同一アミノ酸は白抜き文字で示す。(D) PHドメインのアミノ酸配列表。M1と他のGEF蛋白質および基準となるヒトフレクストリン(pleckstrin)に存在するPHドメインを並列した。同一アミノ酸は白抜き文字で示す。

【図2】新規蛋白質M1の発現を、ラット胎児脳、およびM1 cDNAを組み込んだ発現プラスミドpCDNA3.1 (+)をトランスクレクトしたCOS-7細胞で確認した図面である。図中、レーン1、2はラット胎児脳、レーン3～9は形質転換したCOS-7細胞でのM1発現を示し、形質転換のためのベクターとして、レーン3と4はM1 cDNAを組み込んだベクター、レーン5はコントロールベクター、レーン6と8はHA-タグで標識したM1 cDNAを組み込んだベクター、レーン7と9はHA-タグを組み込んだコントロールベクターを使用した。また、レーン1、3、5は、予め抗M1抗体を対応する抗原であるM1ペプチドで吸収して(p.e.p.+用いた結果である。

【図3】新規蛋白質M1とAPC遺伝子産物とのin vivoでの結合をラット胎児脳溶解物について解析した結果を示す図面である。図中、レーン1および2はラット胎児脳の溶解物を抗M1抗体で、レーン3および4は抗APC抗体で、レーン5および6は抗β-カテニン抗体で免疫沈降した結果、レーン1、3、5は、予め各抗体を対応する抗原で吸収して(p.e.p.+用いた結果である。

【図4】新規蛋白質M1とAPC遺伝子産物との結合部位を説明する図である。+はAPC遺伝子産物との結合活性陽性、-は陰性を表す。\*はAPC遺伝子産物のアルマジロ配列をペイトとした2ハイブリッドスクリーニングで得られたクローニングを示す。

【図5】新規蛋白質M1とRhoファミリー低分子量G蛋白質との結合を示す図面である。

【図6】新規蛋白質M1の低分子量G蛋白質からのGDP解離に対する促進作用を示す図であり、図Aは低分子量G蛋白質Rac1に対する作用、図Bは低分子量G蛋白質RhoAに対する作用を示す。

【図7】新規蛋白質M1の低分子量G蛋白質へのGTP結合に対する促進作用を示す図であり、図Aは低分子量G蛋白質Rac1に対する作用、図Bは低分子量G蛋白質RhoAに対する作用を示す。

【図8】新規蛋白質M1のGEF活性が、APC-アルマジロドメインの添加により増強されることを示す図である。

【図9】新規蛋白質M1とAPC遺伝子産物とが、それらを発現した上皮細胞株中の細胞の辺縁の同一部位に存在することを示す図面である。図中、a、bはHA-タグで標識したM1蛋白質を発現させた同一細胞、c、dはHA-タグで標識したM1蛋白質とMyo-c-タグで標識したAPC-armとを両方発現させた同一細胞、eはHA-タグで標識したM1△NB(アミノ酸127-619)を発現させた細胞、fはMyo-c-タグで標識したAPC-armを発現させた細胞である。また、a、bは抗HA抗体と抗APC抗体で二重染色し、c、dは抗HA抗体と抗Myo-c抗体で二重染色し、eは抗HA抗体で、fは抗Myo-c抗体で処理したものである。b中の矢印頭は、APC蛋白質のクラスターの存在を示しており、また、a～d中の矢印は、M1とAPCの存在を示す。

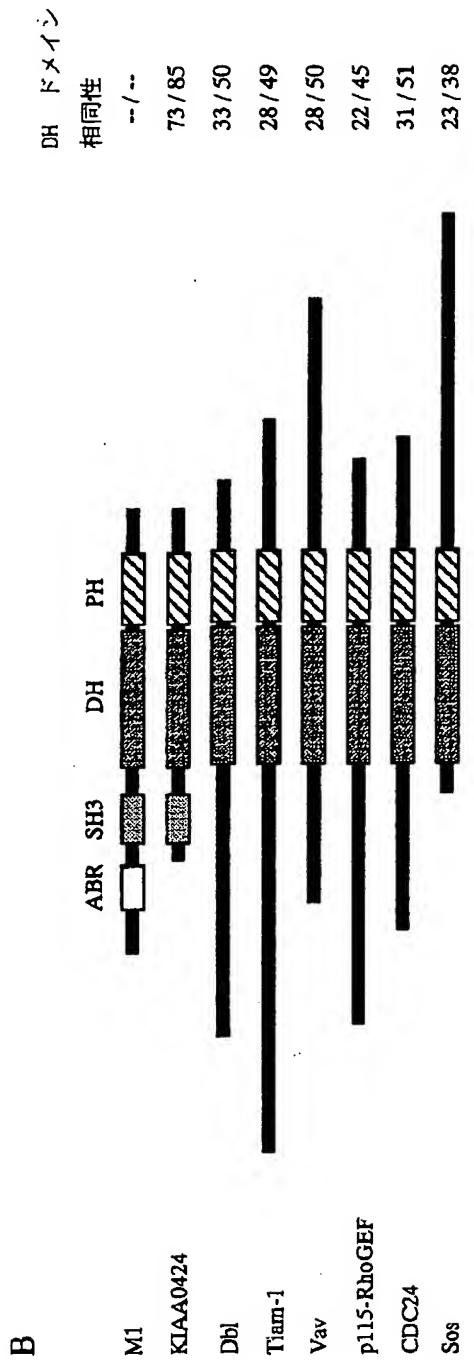
### 【図1】

A

```

MRPDGQQALDAVVRSFDCHSEAALRQRNDVIYCSLPRTAQGIVQREDQL
EVLVS LREVWGRRRGRDGTCTGAMPDGALDTAVCADEVGVSEEDLYDDLH
SSSHHYSHPGGGGEQLAINELISDGSVVCAEALWDHVTMDDQELGFKAG
DVIEVMDATNREWWWWGRVADGEGEGWFPASFVRLRVNQDEPADDAPLAGN
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SLDGFLLTPVQKICKYPLQLAELLKYTHPQHRDFKDVEAALHAMKNVAQ
LINERKKRLENIDKIAQWQSSIEDWEGEDLLVRSSELIYSGELTRVTOP
OAKSOORMFFLFDHOLIYCKKDLLRRDVYYKGRLDMGLEVVDLEDGK
DRDLHVSIKANFRLHRGATGDSHLCTRKPEQKWLKAFAREEQV
DQETGFSITELQRKQAMLNASKQQVTGKPKAVGRPCYLTRQKHPALPSN
RPQQQVLVLAEPRRKPSTFWHSISRILAPFRK*

```



B

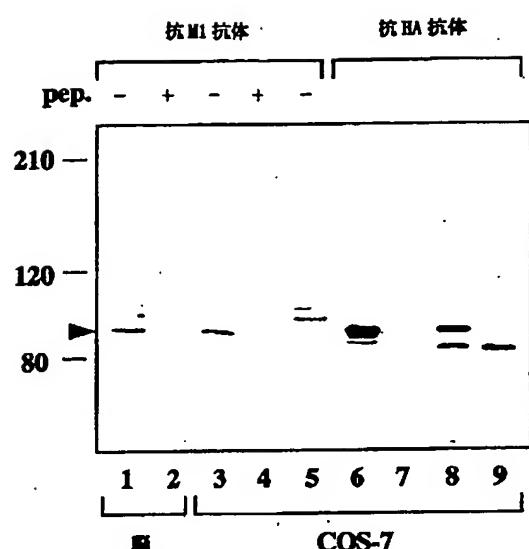
C

M1 KLA0424 215 TN [REDACTED] IGH RDICEGYVRQCRKRAMDFSEEQL RT GIEDIYRCQKA YKA EQRFRNRER HSEL-----  
KLA0424 105 AN [REDACTED] IGH KDICEGYLKQCCRDMFSDQL KV GIEDIYRFOMG VRDEKQYNNDD HSEL-----  
Db1 497 NH [REDACTED] RE ITVLLIGYRAEMDNPEMDMPPLRNRRDIL S MAEIYEFDNDIFLSSLEN-AHA ERV-----  
Tian-1 1,042 RN [REDACTED] NCIMERYLK DKEETFLTQDEL DVL GLTEMVEFOE LKTEGV-RLV DLEKLEKVDFQFKKV  
Vav 196 CCCLR IOQ TDT GS100HFLX DR --FLKQD1 EI IIEDLLRV TH LKEMKEAL GT GAANLYQV-----  
P115RhoGEF 418 Qd1 IS LLV FAKH RM RVLHDLFFQMAECFLFPPEEL ON PSLDELIEV SLIDRMKRRQESGYLIEIGDV-LLARF  
CDC24 280 VKLKTFVA HD PLGDAIDFORRLISLEINA-LVE SKORI-----  
Sos1 202 YDLVKAFMAEIRQ IRE NLIIKVFRF FVSNSKLFS-A NDVEN SRVIDHELSVKKLGHIEDTV-EMTDEGS PHPVGSFCED

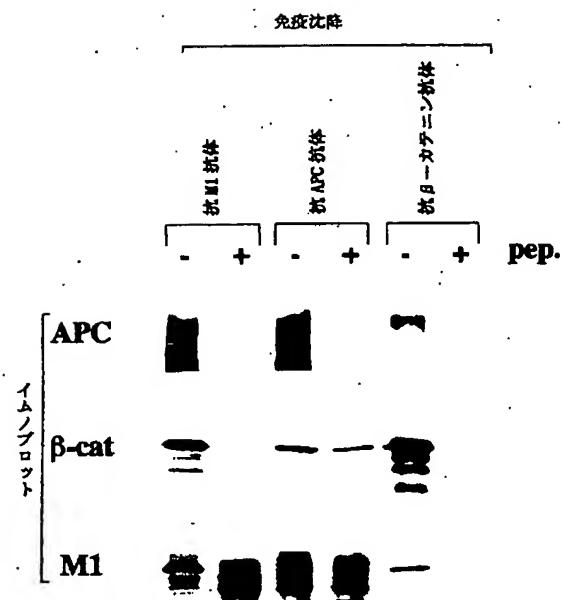
M1 [REDACTED] GACFLEHQADFOI SEYCAHNHNA-CVBLSRBLKLSKYV YFEACRLLQKMDIS DGF LT KICK PQA ALRY  
[REDACTED] GPCFLEHQDGFWI SEYCNHHLDA-CMELSKLMKDSRYQ HFEACRLLQKMDIAIDGF LT KICK PQA ALRY  
[REDACTED] GPCFLERKDDFO AKYCONKPKRSETW RKYSE CAFFOCQR-KLKHRLR DSY LK KICK PQA ALRY  
[REDACTED] LFSLGGSFLYYADREKTI SAFCFA SHTKVPKVLYVAKTDIA KRAFLDAQNPROHSST ESY IR I VLK P R FAL  
[REDACTED] FIKYKERFLV GRYCQSVEASAKHLDVRAAAREDVO MR-LEECQSQRANNGRFT RDL AV M VLK H Q VRH  
[REDACTED] DGAEGSWFOKISSRFCSROSFALLEQKQKORPDR CAFVQAEASPRCRRLO KDMIPTEM LTK P QSIQGN  
[REDACTED] GALEMFHSKHFETKI EPPWSIGONAALEFL SSTLH KMRVDESQRFIINNKLK OSFYK LCR P VK LAE  
[REDACTED] LAAELAF DPYES ARDILRGFGHDRLSQLSKPGRALY LOSIGEGFKEAVQV PRL LA VHCLH FE KQ -EE

M1 KLA0424 [REDACTED] HPOHRDFKDVEA LHAMKNTAOLI RKRRI NIDKIAQ 425  
[REDACTED] AQDHSdryvaa LAYMNTTOOI RKRRI NIDKIAQ-----  
Db1 SKD-CEGSAL [REDACTED] LDAMLDLILKSV DSNHOIAINGYIGNLN-----  
Tian-1 DAESEEYH DV IKTMKYASHI MOKHIEFGAVFD-----  
Vav QEAMEKE-N RL LDAMRDLAQCV VRDN TLRQITN-----  
P115RhoGEF EE-PTEREKYL AECCRELHHV OAVRDMDLRLKD-----  
CDC24 SSD-DNNIKE EA LDISKANLARI NORFJL NHQVVRK-----  
Sos1 KSEDQEDEKE KC ITALLNVQSGEMEKICSKSLAKRRLSESACRFYSQQMKGKQLAIKMNNEIQRNIDGWEGKDIGQC 440

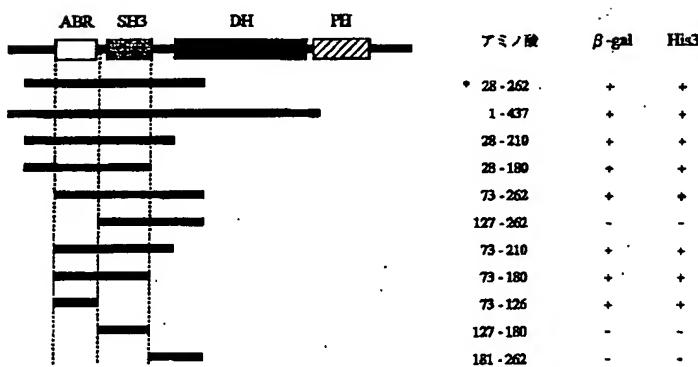
【図 2】



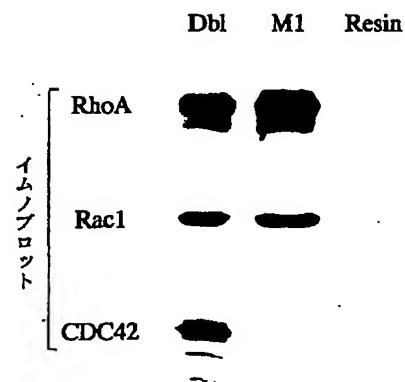
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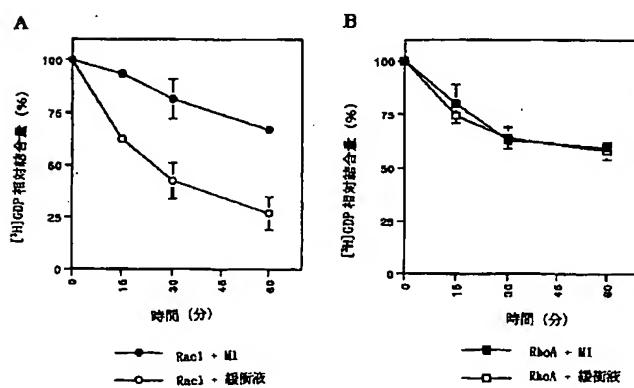
【図 4】



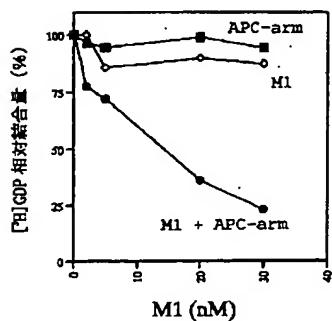
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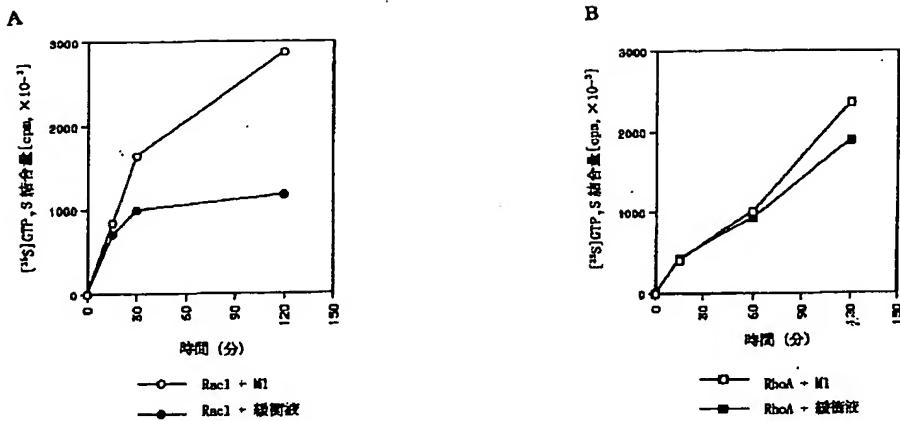
【図 6】



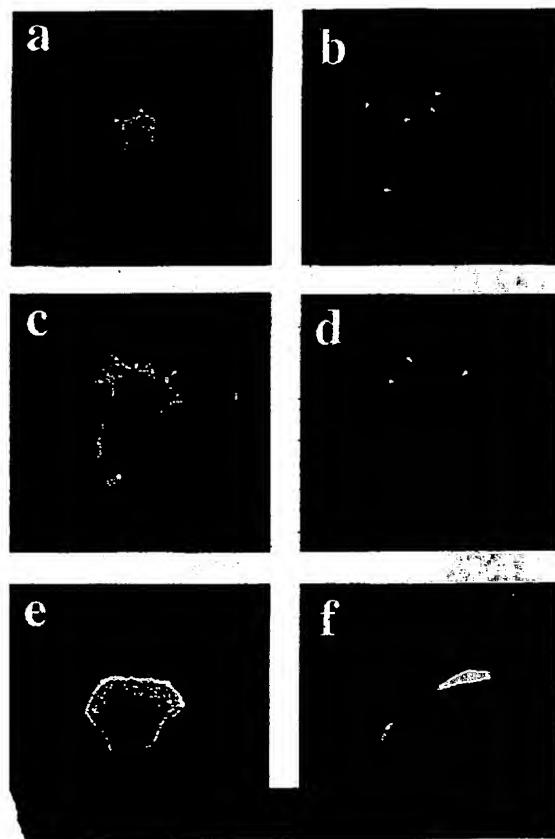
【図 8】



【図 7】



【図 9】



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	1/21	C 1 2 P	21/02	C
	5/10	C 1 2 Q	1/68	A
C 1 2 P	21/02	G O 1 N	33/15	Z
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G O 1 N	33/15			Z
	33/50		33/574	A
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		C 1 2 N	5/00	A

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                   4H045 AA10 AA11 BA10 CA40 DA86  
                   EA50 FA74

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(71) Applicant : DAI ICHI SEIYAKU CO LTD

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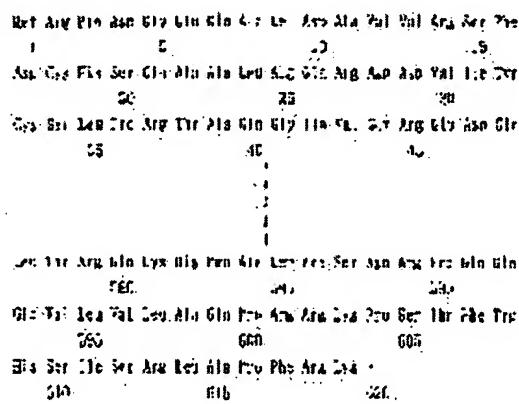
KAWASAKI YOSHIHIRO

## (54) COLON CARCINOMA SUPPRESSOR GENE-RELATED PROTEIN

### (57) Abstract:

**PROBLEM TO BE SOLVED:** To obtain a new protein which has a specific amino acid sequence, has an ability of binding an armadillo repeat site of a gene product of a colon carcinoma suppressor gene, can control the colon carcinoma, and is useful for treating and diagnosing the colon tumor and so on.

**SOLUTION:** This is a new colon carcinoma suppressor gene-related protein which is a polypeptide selected from a group comprising a polypeptide having the amino acid sequence shown by the formula, polypeptides containing the amino acid sequence shown by the



formula, polypeptides having a homology of about 70% or more to [redacted] polypeptide having the amino acid sequence shown by the formula and an ability of binding a polypeptide encoded by the armadillo repeat site of a gene product of a colon carcinoma suppressor gene (Adenomatous Polyposis Coli, APC), and the like, allows the control of APC, and is useful for treating and/or diagnosing the colon carcinoma and so on. This protein is obtained by identifying cDNA of a protein binding an APC gene product from a fetal brain cDNA library for expression.

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#### LEGAL STATUS

[Date of request for examination]

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[Patent number]

[Date of registration]

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[Date of extinction of right]

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CLAIMS

## [Claim(s)]

[Claim 1] Polypeptide chosen from the following group;

\*\* The polypeptide shown in the array number 1 of an array table according to the amino acid sequence of a publication, \*\* The polypeptide containing the amino acid sequence of the polypeptide of the aforementioned \*\*, It has the homology on about 70% of amino acid sequence at least with the polypeptide of the aforementioned \*\*. \*\* And the armadillo repeat part of the gene product of the antioncogene (Adenomatous Polyposis Coli:APC) of colon cancer In the amino acid sequence of the polypeptide which has a binding affinity to the polypeptide which carries out a code, and the polypeptide of the \*\* aforementioned \*\* to \*\* 1 thru/or the deletion of some amino acid, The polypeptide which has variation or induced mutation, such as a permutation and addition, and has a binding affinity to the armadillo repeat part of an APC gene product.

[Claim 2] The polypeptide which has at least five amino acid sequences of the amino acid sequence of a publication for the array number 1 of an array table, and has a binding affinity to the armadillo repeat part of an APC gene product.

[Claim 3] The polynucleotide which carries out the code of the polypeptide according to claim 1 or 2, or its complementary strand.

[Claim 4] The polynucleotide which carries out hybridization to a polynucleotide or its complementary strand according to claim 3 under stringent conditions.

[Claim 5] The polynucleotide in which it is the polynucleotide shown in the array number 2 of an array table according to at least 15 continuous base sequences among the polynucleotide of a publication, or the base sequence of the complementary strand, and the polypeptide discovered by the imprint of this polynucleotide has a binding affinity to the armadillo repeat part of an APC gene product.

[Claim 6] The recombination vector which contains the polynucleotide of a publication in any 1 term of claims 3-5.

[Claim 7] The transformant by which the transformation was carried out by the recombination vector of claim 6.

[Claim 8] The manufacture approach including the process which cultivates the transformant of claim 7 of a polypeptide according to claim 1 or 2.

[Claim 9] The antibody which recognizes immunologically a polypeptide according to claim 1 or 2.

[Claim 10] The screening approach which is the screening approach of the compound which checks or reinforces the affinity over the armadillo repeat part of an APC gene product of a polypeptide according to claim 1, and is characterized by using any one at least among a polypeptide according to claim 1 or 2 and an antibody according to claim 9.

[Claim 11] The screening approach which is the screening approach of the compound which interacts with the polynucleotide of a publication to claim 3 or 4, and checks or reinforces the manifestation of this polynucleotide to it, and is characterized by using any one for any 1 term of claims 3-5 at least among the polynucleotide of a publication, a vector according to claim 6, a transformant according to claim 7, and an antibody according to claim 9.

[Claim 12] The screening approach which is the screening approach of the compound which checks or reinforces the GEF (guanine-nucleotide exchange factor: Guanine nucleotide ExchangeFactor) activity of a polypeptide according to claim 1, and is characterized by using any one at least among a polypeptide according to claim 1 or 2 and an antibody according to claim 9.

[Claim 13] The compound screened by any 1 term of claims 10-12 by the screening approach of a publication.

[Claim 14] The compound which checks or reinforces the affinity over the armadillo repeat part of an APC gene product of a polypeptide according to claim 1.

[Claim 15] The compound which interacts with the polynucleotide of a publication in any 1 term of claims 3-5, and checks or reinforces the manifestation of this polynucleotide in it.

[Claim 16] The compound which checks or reinforces the GEF activity of a polypeptide according to claim 1.

[Claim 17] The physic constituent which is characterized by containing any one at least among the compounds of a publication in any 1 term of a polypeptide according to claim 1 or 2, a polynucleotide given in any 1 term of claims 3-5, a vector according to claim 6, a transformant according to claim 7, an antibody according to claim 9, or claims 13-16 and which is used for the therapy of a large intestine neoplasm.

[Claim 18] The polynucleotide which is the manifestation of the polypeptide of claim 1, or the diagnostic means of the illness relevant to activity, and is carrying out the code of the (a) this polypeptide in a sample, and/or a diagnostic means including analyzing (b) this polypeptide as a marker.

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[Translation done.]

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3. In the drawings, any words are not translated.

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## DETAILED DESCRIPTION

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### [Detailed Description of the Invention]

#### [0001]

[Industrial Application] This invention relates to the new protein (M1 is called hereafter) and the new polypeptide which have a binding affinity to the polypeptide in which the antioncogene (Adenomatous Polyposis Coli:APC) which participates in colon cancer carries out a code, especially a binding affinity to the armadillo repeat part of an APC gene product. The polypeptide which has all or a part of amino acid sequences of the new protein M1 in more detail, The recombination vector containing the polynucleotide which carries out the code of this polypeptide, and this polynucleotide, The manufacture approach of of the peptide or polypeptide using the transformant and this transformant by which the transformation was carried out by this recombination vector, The antibody to this peptide or a polypeptide, the screening approach of a compound of having used these, It is related to the activity inhibition compound which acts on the screened this compound, this polypeptide, or this polynucleotide or an activity activation compound, the physic constituent related to these, and the illness diagnostic means related to these.

#### [0002]

[Description of the Prior Art] Antioncogene APC is isolated as a gene of cause of the familial adenoma nature polyposis (familial adenomatous polyposis:FAP), and the abnormalities of this APC are reported according to 70 - 80% of the colon cancer of sporadicness. An APC gene product is huge protein of 300kDa(s) which consists of 2,843 amino acid (170 Cell, 87:159- 1996). The interaction with various protein is known and an APC gene product has beta-KATENIN in one of them. beta-KATENIN is functioning also as one of the important components of the Wnt/Wingless signal transfer path which bears an important role in a generating process or tumorigenesis at the same time it combines with the cytoplasm side domain of cadherin and it plays a role in cell adhesion (642 Nature, 382:638- 1996). (399 Cell, 86:391- 1996) beta-KATENIN is a kind of oncogene product, and it is thought that the APC gene product demonstrates the cancer control function by controlling the function of beta-KATENIN (1792 Science, 275:1790- 1997). (1787 Science, 275:1784- 1997) (1790 Science, 275:1787- 1997) In addition, as for the APC gene product, the interaction with GSK-3b, Axin, or KONDA cutin / Axil is known (403 Genes Cells, 6:395- 1998). (599 Science, 280:596- 1998) (581 Current Biology, 8:573- 1998) (10826 J. Biol.Chem., 273:10823- 1998) Moreover, the interaction the APC gene product minded the C terminal of EB1 and hDLG is also reported (1023 Science, 272:1020- 1996). Furthermore, it is also known that the armadillo repeat domain which plays a role of the interaction between protein exists in an APC gene product.

#### [0003]

[Problem(s) to be Solved by the Invention] The technical problem which this invention tends to solve is finding out the new matter which participates in the APC gene which is an antioncogene of the colon cancer which bears an interaction with matter various as mentioned above, and is using this new matter as a means aiming at control of cancer. The technical problem of this invention is offering the new matter (M1) with a binding affinity with an APC gene product, especially a binding affinity with the

armadillo repeat domain of the APC gene product origin, and, more specifically, is offering the polypeptide of the useful new matter (M1) origin in connection with it. Moreover, another technical problem of this invention is offering the polynucleotide which carries out the code of the polypeptide of the M1 origin, and offering the manufacturing method of the polypeptide of the M1 origin by the gene engineering technique. Technical problem that this invention is still more nearly another is offering the antibody to the polypeptide of the M1 origin. The technical problem of other this inventions is screening the inhibitor, antagonist, and activator of the operation which M's1 has using the above-mentioned thing, and is offering the screened compound, and is offering the physic constituent and diagnostic means used for the large intestine neoplasm using these.

[0004]

[Means for Solution] For technical-problem solution, this invention person identified cDNA of the new protein M1 combined with the armadillo repeat domain (arm may be called hereafter) of an APC gene product using 2 hybrid screening procedure from the Homo sapiens embryo brain cDNA library, determined the amino acid sequence in which cDNA of the base sequence and this new protein M1 carries out a code, and completed this invention.

[0005] Namely, the polypeptide this invention is indicated to be to the array number 1 of the polypeptide; \*\* array table chosen from the following group according to the amino acid sequence of a publication, \*\* The polypeptide containing the amino acid sequence of the polypeptide of the aforementioned \*\*, It has the homology on about 70% of amino acid sequence at least with the polypeptide of the aforementioned \*\*. \*\* And the armadillo repeat part of the gene product of the antioncogene (Adenomatous Polyposis Coli:APC) of colon cancer In the amino acid sequence of the polypeptide which has a binding affinity to the polypeptide which carries out a code, and the polypeptide of the \*\* aforementioned \*\* to \*\* 1 thru/or the deletion of some amino acid, The polypeptide which has variation or induced mutation, such as a permutation and addition, and has a binding affinity to the armadillo repeat part of an APC gene product; It has at least five amino acid sequences of the amino acid sequence of a publication for the array number 1 of an array table. To and the armadillo repeat part of an APC gene product The receiving binding affinity The polypeptide which it has; the polypeptide of this invention The polynucleotide which carries out a code Or the complementary strand; The polynucleotide of this invention Or the polynucleotide which carries out hybridization to the complementary strand under stringent conditions; It is the polynucleotide shown according to at least 15 continuous base sequences among the polynucleotide of this invention, or the base sequence of the complementary strand. The polypeptide discovered by the imprint of this polynucleotide has a binding affinity to the armadillo repeat part of an APC gene product.

polynucleotide; -- recombination vector; containing the polynucleotide of this invention -- the process which cultivates the transformant of transformant; this invention by which the transformation was carried out by the recombination vector of this invention is included -- The manufacture approach of the polypeptide of this invention; It is the screening approach of the compound which checks or reinforces the affinity over the armadillo repeat part of the APC gene product of the polypeptide of this invention. The screening approach characterized by using any one at least among the polypeptide of this invention, and the antibody of this invention; It is the screening approach of the compound which interacts with the polynucleotide of this invention, and checks or reinforces the manifestation of this polynucleotide. The polynucleotide of this invention, the vector of this invention, the transformant of this invention, Among the antibodies of this invention, at least any one The screening approach characterized by using; It is the screening approach of the compound which checks or reinforces the GEF (guanine-nucleotide exchange factor: Guanine nucleotide Exchange Factor) activity of the polypeptide of this invention. The polypeptide of this invention, Among the antibodies of this invention, at least any one Using It interacts with the polynucleotide of compound; this invention which checks or reinforces the affinity over the armadillo repeat part of the APC gene product of the polypeptide of compound; this invention screened by the screening approach of this invention. screening approach; by which it is characterized -- The compound which checks or reinforces the GEF activity of the polypeptide of compound; this invention which checks or reinforces the manifestation of this polynucleotide; The polypeptide of this invention,

The polynucleotide of this invention, the vector of this invention, the trans-tant of this invention, The physic constituent used for the therapy of the large intestine neoplasm characterized by containing any one at least among the antibody of this invention, or the compound of this invention; They are the manifestation of the polypeptide of this invention, or the diagnostic means of the illness relevant to activity. The polynucleotide which is carrying out the code of the (a) this polypeptide in a sample, and/or a diagnostic means including analyzing (b) this polypeptide as a marker are offered.

[0006]

[Embodiment of the Invention] (New M1) The cDNA is acquired as matter to which the polynucleotide which carries out the code of the new protein M1 offered in this invention uses the armadillo repeat domain of an APC gene product for, and has a new amino acid sequence by 2 hybrid screening procedure from a human embryo brain cDNA library. cDNA of the new protein M1 of this invention carried out the code of the protein which consists of 619 amino acid, and had domain structure similar to a known Dbl family (it is one of the GDP dissociation promotion protein which acts on a low-molecular-weight G protein Rho family) (222 Current Opinion in CellBiology, 8:216- 1996). When the gene database (The National Center for Biotechnology Information) was searched, it became clear that cDNA of the new protein M1 of this invention had the known matter KIAA0424 and about 73% of homology who are one of the Dbl families. KIAA0424 -- the new protein M1 of this invention -- this -- it has the biggest difference at the point lacked in the N terminal region of M1. Both are the same in the point which supports a Dbl homologous (DH) domain, a PUREKKUSUTORIN (Preckstrin) homologous (PH) domain, and Src homologous 3 (SH3) domain. moreover, organization distribution research of the new protein M1 using a mouse -- setting -- this -- it checked that mRNA of M1 was discovered with a high level in the brain, and had discovered other organs by the low.

[0007] The antibody produced using the peptide fragment (amino acid 73-126 of an array table and the array number 1) of the new protein M1 showed strong reactivity to the new protein M1 obtained as a fusion protein with a glutathione-S-transferase (GST). Moreover, the new matter M1 which exists in a brain checked that it was the protein of about 85 kDa(s) by the system of measurement using an antigen-antibody reaction using the produced this antibody.

[0008] Moreover, it sets to the experiment for checking the direct interaction of the new protein M1 and an APC gene product. Although the armadillo repeat domain (APC-arm) of the APC gene product acquired as a fusion protein with a glutathione-S-transferase (GST) interacted with GST fusion M1 fragment (GST-M1-M) With a GST independent, although it did not react but M1-M reacted with GST-APC-arm similarly, it checked not reacting with the armadillo repeat domain of GST fusion beta-KATENIN, or a GST independent. That is, it is presumed that the new protein M1 is combined through the armadillo repeat domain of an APC gene product and this APC gene product. Moreover, it became clear by carrying out immunoprecipitation of the melt (lysate) of a rat embryo brain by the anti-APC antibody, and subsequently carrying out an immuno blot by anti-M1 antibody that M1 of this invention acted to an APC gene product as Mr. [ coprecipitation ] In this reaction, when anti-M1 antibody was pretreated in M1 fragment holding antigenic, the coprecipitation of M1 and an APC gene product was checked. That is, M1 and an APC gene product are considered to have joined together in the living body. Moreover, when the bonding site of M1 and an APC gene product was checked using 2 hybrid methods, it was presumed that a bonding site exists in the field shown from the amino acid 73-126 of M1 at least. This means that a binding site with the armadillo repeat domain of an APC gene product exists in the upstream region of SH3 domain of M1. Since KIAA0424 does not have such a field, it does not have reactivity with an APC gene product.

[0009] Furthermore, it checked that the new protein M1 had specific GEF activity in Rac which is one of the Rho families as the operation. That is, it combines with Rac, and the new protein M1 promotes GDP/GTP exchange reaction, activates Rac, and acts on NFkappaB, c-jun, SRE, etc. which are located in the lower stream of a river of cell signal transduction where Rac involves. Moreover, the RAFFU ring of lame RIPODIA (lobopodium) of a cell or a cell membrane which is the physiological function of Rac may be guided, and the intervention to cell adhesion is presumed.

[0010] about the intracellular localization of an APC gene product, in case a cell moves to a large

intestine villus tip from KURITAIZU, piling up at least the microtubule portion of the cell which moves is reported -- \*\*\*\* (179 J. Cell Biol., 134:165- 1996) -- it found out also accumulating the new protein M1 of this invention on the same part. From this, the new protein M1 of this invention may have grasped the key of the cell migration control in a large intestine villus.

[0011] (Polypeptide) The new protein M1 of this invention is a polypeptide which consists of an amino acid sequence shown in the array number 1 of an array table. Furthermore, the polypeptide of this invention is chosen from the polypeptide which has the partial array of the polypeptide shown in the array number 1 of this array table. The polypeptide chosen has more preferably the homology who surpasses about 90% still more preferably about 80% or more about 70% or more as preferably as the polypeptide shown in the array number 1 of an array table. Selection of a polypeptide with this homology can be performed by making affinity with the armadillo repeat domain of for example, an APC gene product into an index.

[0012] the technique of determining the homology of an amino acid sequence -- the very thing -- it is well-known, for example, the approach of determining an amino acid sequence directly, the method of presuming the amino acid sequence by which a code is carried out to this after determining the base sequence of the polynucleotide presumed, etc. can be used.

[0013] The polypeptide of this invention can use the amino acid sequence chosen from the polypeptide which has the partial array of the polypeptide which consists of an amino acid sequence shown in the array number 1 of an array table as a reagent, the standard substance, and immunogen. As the smallest unit, at least preferably, it consists of an amino acid sequence which consists of about 11-15 or more amino acid at least still more preferably, and about five or more polypeptides [ about 8-10 or more ] which can be screened immunologically are set as the object of this invention at least.

[0014] Furthermore, the polypeptide which consists of an amino acid sequence which has variation or induced mutation, such as 1 thru/or deletion, a permutation, addition of some amino acid, can also be offered by making affinity with the armadillo repeat domain of an APC gene product into an index based on the polypeptide specified in this way. the means of deletion, a permutation and addition, or insertion -- the very thing -- it is well-known, for example, the technique (219:666 Science, 1983) of Ulmer can be used. Furthermore, these peptides that can be used are changeable to extent without remarkable modification of functions, such as embellishing the configuration amino group or carboxyl group etc.

[0015] The polypeptides of this invention are these very thing, and can be used for the physic constituent for adjusting the function of the new protein M1. Moreover, the polypeptide of this invention can be used for the screening for obtaining the compound which can adjust the function of the new protein M1, for example, an inhibitor, an antagonist, an activator, etc., and acquisition of the antibody to the new protein M1. Furthermore, the polypeptide of this invention is usable also as a reagent and a reference standard.

[0016] (Polynucleotide) The polynucleotide in which the peptide which has at least 15 continuous base sequences, and carries out a code has a binding affinity with the arm domain of an APC gene product is meant among the complementary strand to the polynucleotide and this polynucleotide of the array number 2 of an array table to which the polynucleotide of this invention and its complementary strand carry out the code of the amino acid sequence given in the array number 1 of an array table, these polynucleotides and the polynucleotides which carry out hybridization under stringent conditions, and these polynucleotides. If DNA is taken for the example of representation as a polynucleotide, "DNA hybridized under stringent conditions to DNA" can be obtained by the approach of a publication to above-mentioned Molecular Cloning. In the inside of the solution of 0.1xSSC and 0.5%SDS after warming at 42 degrees C here in the solution of for example, 6xSSC, 0.5%SDS, and 50% formamide, saying "high BURITAIZU is carried out under stringent conditions" It means that the signal of electropositive high BURITAIZU is still observed also on the conditions washed at 68 degrees C.

[0017] The polynucleotide of this invention means the homologous chain and complementary strand which carry out the code of the amino acid sequence of a publication to the array number 1 of an array table and which are chosen from the information on the polynucleotide of the array number 2 of an array

table, and means the polynucleotide array which consists of about 15-20 or more arrays at least and this complementary strand corresponding to a field of the specified nucleotide sequence. Manifestation protein can be simply checked using this protein manifestation system with the well-known decision of a useful polynucleotide array, for example, an acellular protein manifestation system, and it can carry out by making that bioactive, especially affinity with the armadillo repeat domain of an APC gene product into an index, and sorting out them. As an acellular protein manifestation system, the technique of the ribosome system of the origins, such as a germ and rabbit reticulocyte, can be used, for example (161 160- Nature, 179, 1957).

[0018] Each of these polynucleotides can provide manufacture of the new protein M1 of this invention, and the polypeptide of this invention with useful gene information, and it can be used for them as the probe or primer for nucleic acids, such as a gene which carries out the code of these, or mRNA detection, or antisense oligomer for adjusting gene expression. For example, when using the polynucleotide of this invention as antisense, the manifestation of M1 is specifically checked by using the nucleotide sequence of a field peculiar to other known protein M1, for example, new protein other than a consensus sequence field with the KIAA0424 grade which is one of the Dbl families. Furthermore, the polynucleotide of this invention can be used also as the reagent and a reference standard about a nucleic acid.

[0019] (Transformant) except for the above acellular protein manifestation systems -- the very thing, such as Escherichia coli, yeast, a Bacillus subtilis, an insect cell, and an animal cell, -- the polypeptide which consists of new protein M1 which consists of this invention, and its origin object with the gene modification technology using a well-known host can be offered. In the example of this invention, although COS-7 cell was used, of course, it is not limited to this.

[0020] a transformation -- the very thing -- a well-known means can be applied, for example, a host's transformation is performed as replicon using a plasmid, a chromosome, a virus, etc. Although the method of integrating into a chromosome will be raised as a more desirable system if the stability of a gene is taken into consideration, the autonomous replication system using an extranuclear gene is used simple. A vector is chosen by host's class and uses as a component the gene sequence which supported the information about the gene sequence, the duplicate, and control for the purpose of a manifestation. a component -- a host -- a prokaryotic cell or an eukaryotic cell -- choosing -- about a promotor and a ribosome bond part -- a terminator, a signal sequence, an enhancer, etc. -- the very thing -- it is combined and used by the well-known approach.

[0021] a transformant -- the very thing -- it can use for manufacture of the polypeptide of this invention by choosing and cultivating the optimal conditions for each well-known host's culture condition. Although the bioactive of the polypeptide which consists of new protein M1 by which manifestation production is carried out, and its origin object, especially affinity with the armadillo repeat domain of an APC gene product may be made into an index and culture may perform them, it makes an index the amount of transformants in a culture medium, and subculture or a batch performs it.

[0022] (Recovery of the new protein M1 and its origin object) Recovery of the polypeptide which consists of the new protein M1 and its origin object from a culture medium makes an index affinity with the armadillo repeat domain of an APC gene product, combines molecular sieving, an ion column chromatography, an affinity chromatography, etc., or can carry out purification recovery also with fractionation means based on a solubility difference, such as an ammonium sulfate and alcohol. More preferably, based on the information on an amino acid sequence, the antibody to this amino acid sequence is created, and the approach of carrying out adsorption recovery specifically by the polyclonal antibody or the monoclonal antibody is used.

[0023] (Antibody) An antibody sorts out and creates the antigenic determinant of the polypeptide which consists of the new protein M1 and its origin object of this invention. At least five antigenic determinants consist of at least 8-10 amino acid more preferably. This amino acid sequence does not necessarily need to be the array number 1 and homologous of an array table, and if an exposed part is only discontinuity, it is [ that what is necessary is just an exposed part to the exterior on a proteinic spacial configuration ] effective [ an amino acid sequence ] that it is also an amino acid sequence

continuous about this exposed part. In the example, the fragment of the pl [ 73rd ] - the 126th place of an amino acid sequence was used as immunogen. An antibody is not limited especially as long as the polypeptide which consists of new protein M1 and its origin object immunologically is recognized. A well-known antigen antibody ligation reaction determines the existence of this recognition.

[0024] In order to produce an antibody, the polypeptide which consists of the new protein M1 and its origin object of this invention is combined with independent or support under existence of an adjuvant or nonexistence, and immunity induction of a humoral response, a cellularity response, etc. is performed to an animal. Support is not limited especially if self does not cause adverse reaction to a host, for example, a cellulose, a polymerized amino acid, albumin, etc. are illustrated. As an animal which carries out immunity, a mouse, a rat, a rabbit, a goat, a horse, etc. are used suitably. a polyclonal antibody -- the very thing -- it acquires by the antibody collecting method from a well-known blood serum. As a desirable means, it is the immunity affinity chromatography method. In the example, the affinity chromatography which combined GST-M1 refined anti-M1 antibody.

[0025] the animal to which the above-mentioned immunity means was given in order to produce a monoclonal antibody to an antibody forming cell -- collecting -- the very thing -- it is carried out by introducing the transformation means to a well-known permanent clonogen.

[0026] A polyclonal antibody or a monoclonal antibody combines with the new protein M1 which consists of direct this invention, is controllable in the activity and can control the interaction system of an APC gene product and the new protein M1 easily. Therefore, it is useful because of the therapy and prevention of the disease to which an APC gene product and the new protein M1 relate.

[0027] The polypeptide which consists of new protein M1 prepared in this way and its origin object, (Screening) The cell to which the transformation of these was carried out based on the information on the polynucleotide which carries out a code and its complementary strand, these amino acid sequences, and a base sequence, The antibody which recognizes immunologically the polypeptide which becomes a list from the new protein M1 and its origin object Independent or the affinity of the polypeptide and APC gene product which consist of new protein M1 and its origin object by combining two or more means, A means effective in screening of the inhibitor or activator to the manifestation of functions, such as the GEF activity of the new protein M1, or the new protein M1 is offered. By namely, the thing of the polypeptide of this invention, and the antibody of this invention for which any one is used at least The screening approach for obtaining the compound which checks or reinforces the affinity of the polypeptide of this invention and an APC gene product The polynucleotide of this invention, the vector of this invention, the transformant of this invention, The screening approach of the compound which interacts with the polynucleotide of this invention, and checks or reinforces the manifestation of this polynucleotide by the thing of the antibody of this invention for which any one is used at least The screening approach of the compound which checks or reinforces functions, such as the GEF activity of the polypeptide of this invention, can be offered by the thing of the polypeptide of this invention, and the antibody of this invention for which any one is used at least. for example, sorting of the antagonist by the drug design based on the spacial configuration of a polypeptide, sorting of the manifestation regulator in the gene level using a protein manifestation system, sorting using an antibody of the antibody recognition matter, etc. -- the very thing -- in a well-known drugs screening system, it is available.

[0028] (A compound, physic constituent) The compound obtained by the above-mentioned screening approach is available as candidate compounds, such as the inhibitor and antagonist which adjust functions, such as an interaction of the polypeptide and APC gene product which consist of new protein M1 and its origin object, or the GEF activity of the new protein M1, and an activator. Moreover, it is available also as candidate compounds, such as the inhibitor and antagonist to the manifestation of the polypeptide which consists of the new protein M1 and its origin object in gene level, and an activator. As candidate compounds, such as the above-mentioned inhibitor, an antagonist, and an activator, protein, a polypeptide, the polypeptide that does not have antigenic, a low molecular weight compound, etc. are mentioned, and it is a low molecular weight compound preferably.

[0029] The candidate compound sorted out in this way can be prepared as a physic constituent used for

the therapy of a large intestine neoplasm by sorting out in consideration of balance of biological usefulness and toxicity. Moreover, these very thing can use the antibody which recognizes immunologically the polypeptide which becomes a vector list including the polypeptide which consists of new protein M1 which consists of this invention, and its origin object, the polynucleotide which carries out the code of these and its complementary strand, and these base sequences from the new protein M1 and its origin object as a physic means used for the therapy of the large intestine neoplasm which has functions, such as inhibition, antagonism, activation, etc. to the interaction of the new protein M1 and an APC gene product Here, specifically with a large intestine neoplasm, the familial adenoma nature polyposis (FAP) and colon cancer are mentioned including a benign tumor and a malignant tumor. in addition -- if in charge of pharmaceutical preparation-ization -- the very thing -- a well-known polypeptide, protein, a polynucleotide, an antibody, etc. should just introduce the pharmaceutical preparation-ized means according to each set elephant.

[0030] The polypeptide which consists of new protein M1 which consists of this invention, and its origin object, In a vector list including the polynucleotide which carries out the code of these and its complementary strand, and these base sequences The antibody which recognizes immunologically the polypeptide which consists of new protein M1 and its origin object It can be used as diagnostic means, such as a disease relevant to the manifestation of the disease M1 to which the manifestation of the polypeptide of this invention or its activity relates, for example, the new protein of this invention, or an interaction with an APC gene product. Especially, it is useful as diagnostic means, such as a diagnostic marker of a large intestine neoplasm, and/or a reagent. A diagnosis is performed determining the abundance of the \*\*\*\*ing nucleic-acid array using an interaction and reactivity with the nucleic-acid array which is carrying out the code of the new protein M1, determining biodistribution about the new protein M1, and/or by determining the abundance in the inside of the sample of the new protein M1. In detail, the new protein M1 is authorized as a diagnostic marker. the measuring method -- the very thing - what is necessary is just to use a well-known antigen-antibody reaction system, an enzyme reaction system, the PCR system of reaction, etc. In addition, the means said here means the approach and/or medium which are used for the purpose achievement. That is, for example, the approach for diagnosing, the reagent kit used for a diagnosis are contained in a diagnostic means.

[0031]

[Example] Hereafter, although this invention is concretely explained based on an example, this invention is not limited to the following example.

(Cloning [ of cDNA ] ) 2 hybrid screening (two hybrid screens) (CLONTECH MATCHMAKER™ Two-Hybrid System) was performed for the purpose of obtaining the protein which has a binding affinity to the armadillo repeat domain (it may be hereafter called APC-arm for short) of an APC gene product. Namely, GAL4 with which the Homo sapiens APC gene product armadillo repeat domain (amino acid residue 446-880) was united as Bate (bait) It screened for the Homo sapiens embryo brain (human fetal brain) cDNA library (Clontech) using plasmid GBT9-APC containing a DNA binding domain. Transfection of this cDNA library and Bate was carried out to the yeast which introduced his3 and lacZ as a reporter gene, and the electropositive clone was detected by making beta-gal assay and HIS auxotroph into an index.

[0032] One electropositive clone was obtained from  $1.1 \times 10^7$  transformants. It was a new array when DNA sequence determined the base sequence of the cDNA fragment which carries out the code of the polypeptide combined with APC-arm discovered by this clone from this obtained clone. The array of the downstream region of the obtained cDNA fragment is 'Marathon'-ready. It acquired by the 3'RACE system (Clontech) using the Homo sapiens brain cDNA (Clontech). The primer used 5'-CGACATCTGCGAGGGCTACGTCCGG-3'. Moreover, it screened by the hybridization which used the digoxigenin (digoxigenin;DIG) indicator probe about the human genome library (Clontech) by using as a probe a part of array (an array table, base number 97-269 of the array number 2) of the cDNA fragment obtained above. Consequently, two clones containing the base number 1-81 of an array table and the array number 2 to overlap were obtained, and the array of the perfect length cDNA of the protein combined with target APC-arm was determined.

[0033] (Amino acid sequence) cDNA shown in the array number 2 of an array table obtained by the above-mentioned approach had the new base sequence. Based on this cDNA, the presumed amino acid sequence of the new protein M1, i.e., the array of the amino acid residue 619 shown in the array number 1 of an array table, was acquired by the translation of the base sequence ( drawing 1 A ).

[0034] (Homology with the existing protein) Using the presumed amino acid sequence of this new protein M1, when homology retrieval using BLAST (The National Center for Biotechnology Information) was performed to the existing database (Genbank), KIAA0424 and 73% of homology who are one of the subfamily members of a Dbl family were accepted ( drawing 2 B and C ). Although both were the same in the point of holding a Dbl homologous (Dbl homology; DH) domain, a PUREKKUSUTORIN homologous (Preckstrin homology; PH) domain, and Src homologous 3 (SH3) domain, to KIAA0424, it became clear that the N terminal region of the new protein M1 did not exist. Consequently, it was checked that the protein M1 of this invention which has the amino acid sequence shown in the array number 1 of an array table is new protein.

[0035] (Check of a manifestation organization) The manifestation in the human tissue of the new protein M1 shown below according to the presumed amino acid sequence of the array number 1 of an array table was checked by NOZAN blotting analysis. a variety -- human tissue -- from -- having obtained -- poly -- ( -- A -- ) -- + -- RNA -- a blot -- having carried out -- a filter -- Clontech -- a shrine -- receiving -- DIG -- an indicator -- having carried out -- M -- one -- cDNA -- a probe -- five -- ' - GACCACACTGCCATCGCTG - three -- ' -- and -- five -- ' - TGTAGTTACCAAGGACCG - three -- ' -- hybridization -- having carried out . Consequently, it checked that it was discovered with a high level in the brain. Moreover, tissue In the analysis by blots, existence was checked also by the testis in addition to the brain. Furthermore, the manifestation was checked also in the cell of the kidney origin.

[0036] (Production of an antibody) Using the peptide containing the amino acid 73-126 of M1, by the well-known approach, immunity of the NZW rabbit was carried out and the antibody to M1 prepared it. Using the peptide containing the amino acid 1122-1729 of an APC gene product (it may call for short Following APC), by the well-known approach, immunity of the NZW rabbit was carried out and the antibody to APC prepared it. The mouse monoclonal antibody to the N terminal region of APC was prepared by the well-known approach (Miyashiro et al.1995). The antibody was refined by performing affinity chromatography using the affinity column which combined the antigen used for immunity, respectively. When the joint reactivity of rabbit polyclonal anti-M1 refined antibody and the refined GST fusion M1 (GST-M1) was investigated, the obtained antibody showed reactivity strong against GST-M1.

[0037] (Manifestation of M1) In order to make the new protein M1 of this invention discover, cDNA of M1 was included in the EcoRI/NotI part of the manifestation plasmid pcDNA3.1 (+), and transfection was carried out to COS-7 cell. Transfection of the vector incorporating M1cDNA, a control vector, the vector incorporating M1cDNA which carried out the indicator with HA-tag, and the vector incorporating HA-tag was carried out to COS-7 cell for the manifestation check of the new protein M1.

Immunoprecipitation was carried out using anti-M1 antibody acquired as mentioned above and anti-HA antibody about the melt of each cultivated transformant, and the melt of a rat embryo brain by which existence of M1 is checked, fractionation was carried out by SDS-PAGE, and, subsequently the immuno blot was performed using anti-M1 antibody and anti-HA antibody. In COS-7 cell and rat embryo brain (lane 1) which carried out the transformation by the vector (lane 3) incorporating M1cDNA, and the vector (lanes 6 and 8) incorporating M1cDNA which carried out the indicator with HA-tag, the manifestation of new protein was accepted clearly and it became clear that the molecular weight was about 85 kDa(s) ( drawing 2 ). moreover, anti-M1 used antibody -- an antigen -- beforehand -- processing (it displaying by pep.\*\* among drawing 2 ) -- new protein was not detected. That is, it was checked that the new protein M1 recognized by anti-M1 antibody had been discovered.

[0038] (Analysis of association in in vivo of M1 and APC) About the rat embryo brain melt, immunoprecipitation was carried out using the rabbit polyclonal antibody to the new protein M1 and APC produced above, and the mouse monoclonal antibody (Transduction Laboratories) to beta-KATENIN, and SDS-PAGE performed the immuno blot after separating each sediment using each

antibody ( drawing 3 ). In lanes 1, 3, and 5, lanes 1 and 2 show the result ( displays by pep.\*\* among drawing 3 ) which absorbed the result to which it is anti-M1 antibody, lanes 3 and 4 are anti-APC antibodies, and lanes 5 and 6 carried out immunoprecipitation of the melt of a rat embryo brain by anti-beta-KATENIN antibody with the antigen which corresponds each antibody beforehand, and was used. The new protein M1 since beta-KATENIN which the APC gene product which M1 which carried out immunoprecipitation by anti-M1 antibody was detected by the anti-APC antibody or anti-beta-KATENIN antibody, and carried out immunoprecipitation by the anti-APC antibody was detected by anti-M1 antibody, and carried out immunoprecipitation by anti-beta-KATENIN antibody is detected by anti-M1 antibody is in. It became clear to have combined with APC and beta-KATENIN also in vivo. [0039] (Analysis of the interaction part of M1 and APC) In order to analyze the APC joint domain of the new protein M1, various deletion mutants (deletion mutant) of M1 were produced by the well-known approach, and two hybrid systems using yeast (yeast) investigated the joint field with APC. Specifically PCR was performed using the following specific primer, cloning of the deletion mutant of M1 was carried out to pGAD424, and fusing with a GAL4 activation domain was created.

5'-ATTTATTGTAGTTACCAAGGAC-3'5'-TGCCTGAAGCACTCTGGGAC-3'5'-  
GACCACACTGCCATCGCTGATG-3'5'-CCTCAGCCGAACGAAGCTGGCTG-3'5'-CTTGCTGC  
TCTGCGCCTCCGC-3'5'-GTGAATCAGGACGAGCCCCGCG-3'5'--'  
GATGTTCCCGAAGATGGTACG-3'5'-ATGCCTGATGGAGCTCTGGAC-3'-- subsequently Fusant with this GAL4 activation domain is set to two hybrid systems, and it is HIS3. auxotrophy and beta-gal The interaction was examined using reporter activity. Consequently, as shown in drawing 4, it became clear that an APC binding site existed in the field of the upstream of SH3.

[0040] (Joint analysis of M1 and Rho family low-molecular-weight G protein) The new protein M1 has KIAA0424 which is one of the subfamilies of a Dbl family, and high homology. A Dbl family is GDP dissociation promotion protein which acts on the Rho family which is one of the low-molecular-weight G protein. Paying attention to homology with the new protein M1 and KIAA0424, association with Rho family low-molecular-weight G protein (small G protein; RhoA, Rac1, CDC42) was investigated for the functional analysis of the new protein M1. The new protein M1 made to stick to a nickel bead RhoA, Rac1, and GST-CDC42, E1A buffer-solution [50mM HEPES containing 0.1%NP-40, pH7.0, 150mM NaCl, 50mM NaF, 5mM EDTA, 1mMDTT, 50microg/mL phenylmethylsulphonyl fluoride (PMSF), 1microg/ml It mixed at 4 degrees C in leupeptin and 1microg /ml aprotinin] for 1 hour, and the coprecipitation Mr. object was detected by immunoblotting. As shown in drawing 5, Dbl used as electropositive control combined with all the used Rho family low-molecular-weight G protein, but the new protein M1 did not combine CDC42, although RhoA and Rac1 were combined.

[0041] (GEF activity of M1) Next, the GEF activity of the new protein M1 was examined. The low-molecular-weight G protein of the [3H] GDP joint mold used in order to investigate GDP dissociation from low-molecular-weight G protein was obtained by incubating each low-molecular-weight G protein of 2pmol at 0.2microM[3H] GDP and 30 degrees C in 20 minutes and in the buffer solution for installation (loading buffer; 20mM Tris-HCl, pH8.0, 3mM MgCl<sub>2</sub>, 10mM EDTA, and 1mM dithiothreitol). It is 375mM in order to prevent dissociation of [3H] GDP from low-molecular-weight G protein. In addition, this mixed liquor was immediately ice-cooled so that final concentration might serve as 18mM(s) in MgCl<sub>2</sub>. [3H] Dissociation of GDP was performed at 25 degrees C by adding the non-indicators GDP, GTP, and M1 with 250 superfluous times to a reaction solution (20mM Tris-HCl, pH8.0, 6mM MgCl<sub>2</sub>, 3.5mM EDTA, and 1mM dithiothreitol) ( drawing 6 A and B). Next, each low-molecular-weight G protein of 2pmol is incubated in 20 minutes and in the buffer solution for installation (loading buffer) at the 0.2microM non-indicator GDP and 30 degrees C in the low-molecular-weight G protein of the GDP joint mold used in order to investigate association of GTP to low-molecular-weight G protein, and it is 375mM. It obtained by adding MgCl<sub>2</sub> so that final concentration may serve as 18mM(s). [35S] Association to the GDP joint mold low-molecular-weight G protein of GTPgammaS was carried out at 25 degrees C by adding [35S] GTPgammaS of 10microM, and M1 to a reaction solution ( drawing 7 A and B). both a dissociation test and a joint trial -- setting -- a reaction -- the ice-cooled 1ml buffer solution for a halt (20mM Tris-HCl, pH8.0, 25mM MgCl<sub>2</sub>, and

100mM(s) NaCl) -- in addition, it stopped. The diluted mixed solution was filtered through the nitrocellulose filter paper, and the buffer solution for a half washed the filter several times. The radioactivity caught on the filter paper was counted. Protein concentration was measured using bovine serum albumin (BSA) as standard protein.

[0042] As shown in drawing 6, the new protein M1 acted on Rac1 which is the low-molecular-weight G protein which can be combined, and GDP dissociation from Rac1 was promoted, but (drawing 6 A) since it did not combine with RhoA, it did not act on GDP dissociation from RhoA (drawing 6 B). moreover, it is shown in drawing 7 -- as -- the new protein M1 -- GTP association to Rac1 -- having promoted (drawing 7 A) -- GTP association to RhoA was not influenced (drawing 7 B). That is, the new protein M1 of this invention acts on low-molecular-weight G protein, and has GEF activity.

[0043] (Operation of APC over the GEF activity of M1) Under existence of APC-arm or nonexistence, at 30 degrees C, the incubation of the [3H] GDP dissociation promotion ability from Rac1 of a joint mold which combined 20[3H] of nM GDP was carried out for 15 minutes, and it was measured about M1 of still more various concentration. APC-arm was added so that it might become 5 times from M1 by the excessive amount and the mole ratio. As shown in drawing 8, the GDP dissociation promotion ability of M1 was reinforced by addition of APC-arm. That is, when M1 combined with APC, it was suggested that GDP dissociation promotion ability is reinforced.

[0044] (Intracellular localization of M1) Next, the intracellular localization of the new protein M1 of this invention was examined. First, Madin-Darby canine Dulbecco's which contains fetal calf serum (FBS) for a kidney (MDCK) epithelial cell stock 10% modified Eagle's It cultivated in medium (DMEM). M1 and M1\*\*NB(amino acid 127-619) cDNA of an overall length carried out sub cloning into the mammalian expression vector pcDNA3.1 (+) which has a CMV promotor. APC-arm which carried out the indicator with plasmid DNA and a pMKITNeo-Myc tag was built by inserting the DNA fragment which is carrying out the code of the partial array of APC (amino acid 446-880) in pMKITNeo which has SRalpha promotor. The manifestation plasmid transfected the MDCK cell according to the user manual using lipofectamine (LipofectAMINE;Life Technologies).

[0045] The MDCK cell was fixed at 4 degrees C for 1 hour using formaldehyde 3.7% in phosphate buffered saline (Phosphate Buffered Saline;PBS). The fixed cell was processed with the tris buffered saline solution (Tris Buffered Saline;TBS) which contains a triton X-100 0.2% for 10 minutes at a room temperature, and was washed 3 times in TBS. After transparency-izing a cell (permeabilize), it incubated at the primary antibody and the room temperature 3% for 1 hour all over 1%BSA, and FBS and TBS which contains a triton X-100 0.2%. The primary antibody was removed and the cell was washed 3 times in TBS. The united primary antibody was detected using the goat second antibody (Cappel) which combined FITC (Fluorescein isothiocyanate) or a rhodamine. The dyed sample was observed under the KARUTSU ice LSM510 laser scanning microscope (Carl Zeiss LSM510Laser scanning microscope).

[0046] A result is shown in drawing 9. The same cell which made M1 protein which carried out the indicator of a and the b with HA-tag among drawing 9 discover, The same cell which made both of APC-arm which carried out the indicator with M1 protein which carried out the indicator of c and the d with HA-tag, and a Myc-tag discover, The cell which made M1\*\*NB (amino acid 127-619) which carried out the indicator of the e with HA-tag discover, and f are the cells which made APC-arm which carried out the indicator with the Myc-tag discover. Moreover, the double stain of a and the b was carried out by anti-HA antibody and the anti-APC antibody, the double stain of c and the d was carried out by anti-HA antibody and the anti-Myc antibody, e is anti-HA antibody and f was processed by the anti-Myc antibody. As the arrow-head head in b showed, it existed in the film which the cluster of APC protein is elongating and the arrow head in a-d showed, it became clear that M1 and APC lived together to the same part of the verge of a cell in an epithelial cell.

[0047] (Gestalt analysis of M1 manifestation cell strain) The MDCK cell strain which discovers M1\*\*NB to stability was established further, and when the effect which M1 has on the gestalt of a cell and a frame was investigated, the inclination which pastes up densely no M1\*\*NB manifestation cell strain 5 clones, but is increased scatteringly was seen. The intervention to the cell adhesion of the new

protein M1 was presumed.

[0048]

[Effect of the Invention] As explained above, M1 of this invention is new protein, and affinity with the armadillo repeat part of the APC gene product characterizes it, and it has GEF (guanine-nucleotide exchange factor: Guanine nucleotide Exchange Factor) activity. Offer of the new physic constituent and the medical-examination means which this property was used offers big usefulness in the medical field of an APC gene product-related clinical and a foundation.

[Layout Table]

Sequence Listing<110> Daiichi Pharmaceutical Co.,Ltd.<120> Colon carcinoma suppressor gene related protein<130> DP99-1045<160> 2<210> 1<211> 619<212> PRT<213> human<400> 1Met Arg Pro Asp Gly Gln Gln Ala Leu Asp Ala Val Val Arg-Ser-Phe 1 5 10 15 Asp CysHis Ser Glu Ala Ala LeuArg Gln Arg Asn Asp Val Ile Tyr 20 25 30 Cys Ser Leu Pro Arg Thr Ala Gln Gly Ile Val Gln Arg Glu Asp Gln 35 40 45 Leu Glu Val Leu Val Ser Leu Arg Glu Val Trp Gly Arg Arg Arg Gly 50 5560 Arg Asp Gly Thr Cys Thr Gly Ala Met ProAsp Gly Ala Leu Asp Thr 65 70 75 80 Ala Val Cys Ala AspGlu Val Gly Ser Glu Glu Asp Leu Tyr Asp Asp 85 90 95 Leu His Ser Ser His His Tyr Ser His Pro Gly Gly Gly Glu100 105 110 Gln Leu Ala Ile Asn Glu Leu Ile Ser Asp Gly Ser Val Val Cys Ala 115 120125 Glu Ala Leu Trp Asp His Val Thr Met Asp Asp Gln Glu Leu Gly Phe 130 135 140 Lys Ala Gly Asp Val Ile Glu Val Met Asp Ala Thr Asn Arg Glu Trp 145 150 155 160 Trp Trp Gly Arg Val AlaAsp Gly Glu Gly Trp Phe Pro Ala Ser Phe 165 170 175 Val Arg Leu Arg Val Asn Gln Asp Glu Pro Ala Asp Asp Asp Ala Pro 180 185190 Leu AlaGly Asn Ser Gly Ala Glu Asp Gly Gly Ala Glu Ala Gln Ser 195 200 205 SerLys Asp Gln Met Arg Thr Asn Val Ile Asn Glu Ile Leu Ser Thr 210 215 220 Glu ArgAsp Tyr Ile Lys His Leu Arg Asp Ile Cys Glu Gly Tyr Val 225 230 235 240 Arg Gln Cys Arg Lys Arg Ala Asp Met Phe Ser Glu Glu Gln Leu Arg 245 250 255 Thr-Ile-Phe-Gly-Asn Ile Glu Asp Ile Tyr-Arg-Cys-Gln-Lys-Ala-Phe 260 265 270 Val Lys Ala Leu Glu Gln Arg Phe Asn Arg Glu Arg Pro His Leu Ser 275280 285 Glu Leu Gly Ala Cys Phe Leu Glu His Gln Ala Asp Phe Gln Ile Tyr 290 295 300 SerGlu Tyr Cys Asn Asn His Pro Asn Ala Cys Val Glu Leu Ser Arg 305 310 315 320 Leu Thr Lys Leu Ser Lys Tyr Val Tyr Phe Glu Ala Cys Arg Leu 325 330335 Leu Gln Lys Met Ile Asp Ile Ser Leu Asp Gly Phe Leu Leu Thr Pro 340 345350 ValGln Lys Ile Cys Lys Tyr Pro Leu Gln Leu Ala Glu Leu Leu Lys 355 360 365 Tyr Thr His Pro Gln His Arg Asp Phe Lys Asp Val Glu Ala Ala Leu 370 375 380 His Ala Met Lys Asn Val Ala Gln Leu Ile Asn Glu Arg Lys Arg 385 390 395400 LeuGlu Asn Ile Asp Lys Ile Ala Gln Trp Gln Ser Ser Ile Glu Asp 405 410 415 Trp Glu Gly Glu Asp Leu Leu Val Arg Ser Ser Glu Leu Ile Tyr Ser 420 425 430 Gly Glu Leu Thr Arg Val Thr Gln Pro Gln Ala Lys Ser Gln Gln Arg 435 440 445 Met Phe Phe Leu Phe Asp His Gln Leu Ile Tyr Cys Lys Lys Asp Leu 450 455 460 LeuArg Arg Asp Val Leu Tyr Tyr Lys Gly Arg Leu Asp Met Asp Gly 465 470 475480 Leu Glu Val Val AspLeuGlu AspGly Lys Asp Arg Asp Leu His Val 485 490 495 Ser Ile Lys Asn Ala Phe Arg Leu His Arg Gly Ala Thr Gly Asp Ser 500 505 510 His Leu Leu Cys Thr Arg Lys Pro Glu Gln Lys Gln Arg Trp Leu Lys 515 520 525 Ala-Phe-Ala-Arg-Glu Arg Glu Gln Val Gln-Leu-Asp-Gln-Glu-Thr-Gly 530 535 540 Phe Ser Ile Thr Glu Leu Gln Arg Lys Gln-Ala Met Leu Asn Ala Ser 545 550555 560 Lys Gln Gln Val Thr Gly Lys Pro Lys Ala Val Gly Arg Pro Cys Tyr 565570 575 Leu Thr Arg Gln Lys His Pro Ala Leu Pro Ser Asn Arg Pro Gln Gln 580 585 590 Gln Val Leu Val Leu AlaGluPro Arg Arg Lys Pro Ser Thr Phe Trp 595 600 605 His Ser Ile Ser Arg Leu Ala Pro Phe Arg Lys \* 610 615 620 <210> 2 <211> 1860 <212> cDNA <213> human <400> 2 atg agg cca gat ggg cag caa gct ttg gat gct gtg gta agg agt ttt 48 Met Arg Pro Asp Gly Gln Gln Ala Leu Asp Ala Val Val Arg Ser Phe 1 5 10 15 gac tgt cac tct gaa gcagct ctc agg cag agg aat gat gtg att tat 96 Asp Cys His Ser Glu Ala Ala Leu Arg Gln Arg Asn Asp Val Ile Tyr 20 25 30 tgt agt tta cca agg acc gct cag ggt att gtg cag agg gaa gac cag 144 Cys Ser Leu Pro Arg Thr Ala Gln Gly Ile Val Gln Arg Glu AspGln 35 40 45 ctg gag gttctt gtg tca ctc cgt gaa gtg tgg ggg cggcgg agg ggc 192 Leu Glu Val Leu Val Ser Leu Arg Glu Val Trp Gly Arg Arg Arg Gly 50 55 60 aga gat ggg acc tgc act gga gcc atg cct gatgga gct ctg gac aca 240 Arg Asp Gly Thr Cys Thr Gly Ala Met ProAsp Gly Ala Leu Asp Thr 65 70 75 80 gct gtc tgc gct gac gaa gtg ggg agc gag gag gac ctg tat gat gac 288 Ala Val Cys Ala Asp Glu Val Gly Ser Glu Glu AspLeu Tyr Asp Asp 85

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